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: DRGANISM: Homo Sapien
US-10-121-062-166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-121-062-166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID No 219
                                                                                                                                                                                                                                                       Duery Match 16.00 Pred. No. 8.5e-06; Best Local Similarity 40.00 Pred. No. 8.5e-06; Matches 49; Organization 12; Mismarches 36; Indels Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugnance 166. Application US/10121062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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PRIOR APPLICATION TEMPORALS OF FILS WELFTS OF FILL NUMBER OF SECULD NOS: 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER 73,73,721,761
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER.
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                                                                                                                                468 VELIEVSKSEAVALLKKTSSSIVLKALEVKEYERQ 502
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                                                                                                                                                                                                                       105 HPRVVELPK-TDEGLOFNVMGG----KEQNSPIYISKIIFGGVAERHGGLKRGDQLLSVNG 160
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                                    161 VSVEGEHHEKAVELIKAANDSVKL----VVKYLEK 191
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Stewart, Timothy A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski, Paul J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lumas, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                            12.6%; Score 148; DB 6; Length 632;
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; LENGIH: 227
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; TITLE OF INVENTION: Colon and Colon Cancer Associated Polymerlectides and Polypept
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SOFFWARE: pt_FL_qenes Version 6.0 SEQ ID No 266
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18 9 ATTICKT 0 PUPPE PT, TO 1/20020

18 18 ATTICKT 0 NAMED 9-23

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: US 60/164/280
                                                                                                                                                                     APPLICANT: Wend, Gezhi
11111 of INVENTION: Resel Bucheleic Acids and
FILE REFERENCE: 816
CURRENT ADDITIONAL NUMBER - DS/MO/OCS, 204
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                                                                                       CURRENT FILLING PARE: 2002-09-14
NUMBER OF SEQ ID NOS: 728
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NUMBER OF SEQ ID NOS: 8564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 VELTEVSRSEAVALLEKTESSIVLEALEVEEYEPQ 97
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Zhou, Ping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao, Qing A.
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: INCYTE GENOMICS, INC. APPLICANT: DAFFO, Abel
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Local Similarity 34.2%; Pred. Ro. 2e 06;
hes 50, conservative 20; Mismatches 55, Indels 12,
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DAHL, Christopher R.
                                                                                                                                                                                                                                                                                                                                                                                     DAFFO, Abel
GERSTIN, JR
                                                                                                                                                                                                                                                                                                 GIETZEN, Darryl
                                                                                                                                                                                                                                                                                                                                                                     JONES, Anissa L.
                                           NGUYEN, Duy-Viet An
                                                                                                              DAUGHERTY, Sean C
                                                                                                                                       AMSHEY, Stefan R.
                                                                                                                                                                                    TUASON, Olivia
                                                                                                                                                                                                                           HILLMAN, Jennifer L.
                                                                                                                                                                                                                                                      DUFOUR, Gerard E
                                                                                                                                                                                                                                                                              NNIHO
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                                                                     Tommy F
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Edward H.
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LENGTH: 583
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Best Local Similarity
                                                                                                                                                                                                                                           APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P.
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                                              APPLICANT:
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                                                                            Goddard,Audrey
Godowski,Paul J.
Grimaldi,J.Christopher
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LEWIS, Samantha A.
                             Napier, Mary A.
                                                           Gurney, Austin L.
                                                                                                                            Gerritsen, Mary E.
                                                                                                                                             Gerber, Hanspeter
                                                                                                                                                             Fong, Sherman
                                                                                                                                                                          Ferrara, Napoleone
                                                                                                                                                                                                           Desnoyers, Luc
                                                                                                                                                                                                                              Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERALTA, Careyna H.
                                                                                                                                                                                             Eaton, Dan L.
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Paoni, Nicholas F.
               Pan, James
                                               Kijarin, Irar J
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25.2%; Pred. No. 6.9e-06;
Julive 41; Mismatches 67, Indels 45; Gaps
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US 10-106-698-4937
Sequence 4947, Application US/10106598
CONDERAL INFORMATION:
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                                                                                                                                                                 Query Mitch 13.19 90.50 177 (gcf)
Best Local Similarity 36.6%; Pred, No. 4.3e-07;
Matches 37 Conservation 21: Mismatches 25
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SEQ ID No. 4927
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LITLE OF INVENTION: Color and Color Cabbur Associated Polycoclarides and Folytelide
File Reference: PA00501
CURRENT APPLICATION NUMBER: US/10/186,698
CURRENT FILMA DATE: 2022-03-22
PRIOR APPLICATION NUMBER: PUT/US00/26524
PRIOR PRIOR PATE: 2029-99-28
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CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: 60/226/243
PRIOR FILING DATE: 2000-08-17
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HILLE OF INVENTION: HERAPEULIC COMPOUNDS FOR OVARIAN CANCER
FILE REFERENCE: 67 2104.00
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ORGANISM: Homo sapiens
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135 SRILPG WAFRHOOLKEGUOLLSVNGVSVEGEHHEKAVELL 175
                                                   176 APASAPQNVESTIVSSOVNIKKIONEN NIGIKKOTPONOSSILISELVITOS---SAPIVA 2/2
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                                                                                                             86 ARATAKATYAAFAASEGHSHPRV-----VELPKTDEGLGFNV------MGGKEONSPIYI 134
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RESULT
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; Sequence 479, Application US/10102806 ; GENERAL INFORMATION:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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; TYPE: PRT; GRGANISM: Homo Sapien US-10-119-480-76

Guciy Match Hest Local Similarity 78.5%, Pred. No. 3.4e-65; Natches 177, Concernative 24, Mismatches 17, Indels 2, Gaps

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12, ,	626,	Sequence 17, Appl	2027,	£езјасное 281, ∧рр	640,	Separate Till Appl	18,	20,	93, 4	Sequence (47, App	Sequence 712, App	Sequence 533, App	5965,	Sugarance 456, App		266,	Sequence 5902, Ap	Sequence 166, App	₹1°,	Sequence 591, App	Sequence 475, App	Sequence 5822, Ap	493	Sequence 2, Appli	Sequence 76, Appl	Description

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134 TSR I I PAZVAGERBOGIK BODQIL SVNOVSVEGERBREKAVEL I KAAKDSVKI, VVRVI DRVI. 193 113 TSR I I PAZVAGERBON KROLQI I SVNOVSVERDAREKAVILI KAAQOSVKI, VVRVI DRVI. 178

ань мисцетс		Application us/10119480  Application us/10119480  MATION:  Daker, Kevin P.  Deshoyers, Luc Gerritson, Mary  Goddard, Addrey  Goddswski, Paul J.  Grimafdi, Paul J.  Grimafdi, Paul J.  Grimafdi, Paul J.  Grimafdi, Paul J.  Smith, Victoria	Application US/101 MATION: Dashoyers, Luc Ger Gosdard, Andrey Gedewski, Paul J. Grinaldi, J. Chris Grinaldi, J. Chris Grinaldi, J. Chris Smith, Victoria Stephan, Jean-Phil Matunabe, Colin L. Wood, William I.	ion US,  vin P.  vin P.  vin P.  vin P.  paul  paul  paul  Austin  actors  actors	76 Application us/10119480 RMATION: BAKOT, Kevin P. Desmoyers, Luc Gerritsen Gestwaki, Paul J. Gerinaldi, J. Christopher Gittey, Austin L. Gittey, Austin L. Stephan, Jean-Philippe F Matanabe, Colin L.	ENR O T	RESULT 1 Sequence 76 GENERAL INF APPLICANT: A PPLICANT: A PPLICANT
		ALIGNMENTS					
352, App	Seductive	POT US02 09671 352		12 1 12 1		:0 : (n :	(n 4
1558, Ap		PCT - US02 - 096 / 1 - 1368		1400	7.4	х ox л or	2 4 2 4
432, App		US 10 103 313 432		1 44 0 10 10 10	ا- ن دند	86.5	<b>4</b>
10, Appl	-	US-10-109-886-10		2442	7.4	87	. A.
647. App		PYT US02 09671 647		12441	7.4	87	* <u>*</u>
645, App		PCT-USU2-09671-645		2442		87	99
633, App		PCT-US02-09671-633		2442	7.4	87	386
631, App	Sequence	PCT-US02-09671-631		2442	7.4	87	37
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; SEQ ID NO 191322
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: Sequence 191322, Application US/09270849E
: GENERAL INFORMATION:
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LENGTH: 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
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                                                                                                                  81 CPEEFAHATAKATVAAFAASSSHSHPPVVF! PKTSSCLCENVMCCKEGNSP1Y1SKITPG 140
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                                                                                                                                                                                      15 EPLTLSRDVKRSIELLEKLOASODFPTTKLAALOKVLNSDEMTSVREVYEHVYETVDIOG 74
                                                                                                                                                                                                                              21 QPITTIPHOVAMATELLEKTGESGEVPVHETGSTEKVLGSEEGTALHEVYVYHHETITVNG 80
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Search completed: May 7, 2002, 12:43:57 Job time: 211 sec

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; Sequence 17076, Application US/09614150
; GENERAL INFORMATION:
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                                                                                                                                          PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILINC DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: CL900728
CURRENT APPLICATION NUMBER: US/704/614,150
CURRENT FILING DATE: 2909 07 11
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TABLE OF INVENTION: APPAYS, FOR DETECTION EXPRESSION OF 10,000 OF MORE
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NUMBER OF SEQ ID NOS: 30973
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PRIOR APPLICATION NUMBER: 60/184,831
                                            PRIOR APPLICATION NUMBER: 60/175,693 PRIOR FILING DATE: 2000-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/157,832 PRIOR FILING DATE: 1999-10-05
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NUMBER OF SEQ ID NOS: 62517
SOFTWARE, Falcentin Vel. 2.0
SEQ ID NO 33346
LENGTH: 204
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PRIOR APPLICATION NUMBER: 60/191,637
FRIOR FILLY DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                     194 HAWAWATANA GAANTANSTANTANTANTANA ABANABANASANASTITTAN HAMATANA ABATANTAN ABATANTAN
                                                                                        501 GALKIAKKKY 210
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                                                                                                                                                                                                                                                                    141 CVAERECCLEEGF@LLSVNGVSVEGEHHEKAVELLKAAKUSVK..VVS1 FEKVLEDBLASE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 CHEUNARATAKATVAAFAASIGIISIII WVVIIII KIDEGIIGEWVMGGKEQNSPIYISKII PG 140
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                                                                                                                                                                                                                                                                                                                                                                           75 SHOVRASATAKATVAAFAASEGHAHFRVVELPKTEEGLGENVMGGKEGNSFIYISRIIFG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148;
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                                                                                                                                                                                                                                                                                                                                                                                                                            64.4%; Score 754, DB 16, 77.9%; Pred. No. 1.5e-61; attive 20; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16, Length 204;
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RESULT

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: NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSEQ for Wind
: SEQ ID NO 369
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US-60-173-464-14024
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: GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 601\,
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Best Local Similarity 82.1%; Prod. No. 7.4c-65;
Matches 151; Conservative 21; Mismatches 12; Indels
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ORGANISM: HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                            342 GLEFGDOGL SVMGVSVEGEHHEFAVFLLKAAQGEVELVVFYTDEVLEEMESREEKMESAE 401
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GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION. NUCLEIC ACID DETECTION KITS COMPRISING
TITLE OF INVENTION. GENE SEQUENCES EXFRESSED FROM THE DESCOPHILA GENERAL, AND
TITLE OF INVENTION. USES THEREOF
FILE REFERENCE: CL000392
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; SEQ 15 NO 14024
; LENGTH: 195
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: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 17123
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US-60-173 164 14024
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRERT APPLICATION NUMBER, 03/60/151,637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE, PET
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                                           14) AND TARBELLIAM TARBELAND TARBETTE AND ASSESSED TO THE TOTAL TARBETT OF THE TA
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                                                                                                                                             66 SHDVRASATAKATVAAFAASESHAHERVVELEKTEST GENVMSJKEQUSETVISETIET 125
                                                                                                                                                                                                                                                     81 OPERARATAKATVAAFAASECHSHPPVVELDETDEGLJENVMGGEEQNSPIYISKIIFG 140
                                                                                                                                                                                                                                                                                                                                                                                                              21 QPUTILDREVARATEILLERI,QESGEVFVHKT,QSLKKVT,QSDFCTATREVYQYMHDHTVNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 CPEERAPATAKATVAAFAASECHSHPRVVELPKTEECLGENVMCCKEQNSETYISRITPG 140
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                                                                                                                                                                                                                                                                                                                                                                  EPLILSRUVKRSIELLEKLOASGDEPTIKLAALQKVLNSDEMTSVREVYEHVYETVDIQG 65
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148;
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Similarity 77.9%, Pred. No. 1.4e-61;
48; Conservative 29; Mismatched 22; Endels (
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indels 0; Gaps
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SOFTWARE: PERL Program
SEQ ID NO 19
LENGIH: 207
                                                                                                                  SEQ ID NO 19
LENGIH: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Overy Match 69.0%; Score 807; DB 1; Length 207: Hest Local Similarity 78.5%, Fred. No. 1.7e 66, Matches 157; Conservative 24; Mismatches 17; Indelo
                                                                                                                                                                                                                                         APPLICANT: Yue, Henry
APPLICANT Tang, Y. Tom
AFFLICANT Lal, Freeti
APPLICANT Lal, Freeti
APPLICANT Lal, Freeti
APPLICANT Dathers, well
APPLICANT Patterson, Chandra
APPLICANT Baudha, Mariath R.
APPLICANT Lu, Dyand Aina M.
APPLICANT Shah, Furvi
APPLICANT Shah, Furvi
APPLICANT AU-Young Janice
Title OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESTON MOTORTHES
FILE REFERENCE: PF-0760 P
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APPLICANT:
OTHER INFORMATION. Incyte identific No. 4002841301 60-172-354-19
                                                                                                                                                                               CURRENT APPLICATION NUMBER, US/AO/172, 854
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 40
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PRIOR APPLICATION BUNBER, 60,772-952
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                                                                                                                                                             SOFTWARE: PERL Program
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                                      NAMESKEY: misc_feature
                                                        FEATURE:
                                                                       ORCANISM: Homo sapiens
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                                                                                                   TYPE: PRT
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SEQ 10 NO 59
1 LENGTH: 406
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                                                                                                                                              : Sequence 369, Application US/60229518; GENERAL INFORMATION:
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                                                                                                                                                                                                   US:60-229-518-369
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U8:60 213 163 59
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TITLE OF INVENTION: ISOLARD HUMAN PHOSPI
TITLE - INVENTIAL RUCLED ALL M-LEGAL
TITLE - INVENTIAL AND USES THEREOF
FILE REFERENCE: CL000778
CURRENT APPLICATION HUMBER, 05/50/219,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.9%; Score 794; DB 24; Length 406; Best Local Similarity 82.1%; Pred. No. 7.4e-65; Matches 151; Conservative 21; Mismatches 12, Indels
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                                                                                                                                                                                                                                                                                                   102 SECO 405
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                                                                                                                                                                                                                                                                                                                                                                                               342 CHREGORLLEVNGVSVECEHHEKAVELLRAAQGEVELEVRY FEEVLEEMESKEEEMRSAK-401
                                                                                                                                                                                                                                                                                                                                                                                                                     *48 () EPÖ-ÇILSENBÜYSENDERINEAAYBILKAARD SAZILYYYYITEVLEEMSAY BELLPTAN 207
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                                                                                                                    Beasley, Ellen
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                                                                         ISOLATED HUMAN PROSPHATACE PROTEINS, RUCLUES ACTE M. LICULES ENCOURTES HUMAN FIRAGE HATASE A NOTEINS.
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CURRENT FILING DATE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US01-04098A-1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Omery Match 69.6%; Score 814; 18-1; Length 197; Best Local Similarity 80.6%; Pred. No. 3.6e-67; Matches 154, Conservative 24, Mismatches 15, Indees
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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FRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DAIR: 2000-04-27
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PRIOR APPLICATION NUMBER: 09/654,936
PRIOR FILING DATE: 2000-09-01
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/663,561
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CURRENT APPLICATION NUMBER: PC:08831854358A
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115 No 1554
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                                                                                                                                                                 66. OPEFRAFATAKATVAAFAASEGHSHFRVVELEKTGEGGGENVAGCKEGNSETYTSRTIPG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                         21 QPITIOHOVARALFITERIÇESTEVEVERIQSIKAVLQSEKTTAIREVYQYMHETITVNG 80
                                                                                                                                                                                                                                                                                                                                                 6 EPVKLEKDICKAIFII FKI QESOFVPPQKI QALQEVI QSEFONAVREVYEHVYETUDISS 65
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Host Local Similarity 80.6%; Prod. No. 5.60-67;
Matches 154; Conservative 24; Mismatches 15; Indeks
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SUFTWARE: Custom
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ORGANISM: Homo supiens
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                                                                       | Helelell | Helelel | 197
                                                                                                                                                              127 GJADRIGGUR KGIPÇELEN NGVEN EKOLEHHERAN BULKAAN, GEN KLUVEN JOKN LEEMESKE
                                                                                                                         201 EKLKTAKRRÇÇ 211
                                                                                                                                                                                                                        141 GVAFFHOGLEFGLIÐLI SVNIVSVFOFHHEFAVELLEAAEDSVELVVÞYTÞFVLEEMEARF 200
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Z EPVKLEKAIGKALEILEKAAJASEVI FAKKAAJARVIJASERVINAVHEVIBIVITETVILI VOISS 66
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61-0860-35800-134

: Sequence 19, Application PC/TUS0032990 : GENERAL INFORMATION:

INCYTE GENOMICS, INC

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

APPLICANT:

YUE, Henry
AZIMZAI, Yaida
LARG, Y. Tom
PATTERSON, Chandra
EAUCHN, Mariah R.
LU, Dyung Aina M.

APPLICANT:

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Fost-processing: Minimum Match 0% Maximum Match 100%
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Pertect score:
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Maximum DB seq length: 2000000000
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Pending_Patents_AA_Main:*
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Gepyright (e) 1993 - 2000 Compugen Utd.
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Result
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US-60-191-681-1677 US-60-191-681-1677 US-90-4814-180-2094 Characteristics (Co. 100-100) US-60-161-992-1922 VS-61-161-992-1922	08-60-172-354-19 08-60-171-18-18-59 08-60-213-163-59 08-60-213-163-59 08-60-167-245-601 08-60-167-245-601 08-60-167-245-601 08-60-173-681-18-59 08-60-191-681-18-59 08-60-191-681-18-59 08-60-191-681-18-59 08-60-191-681-18-59 08-60-270-767-32-318 08-60-270-767-32-318 08-60-270-767-32-318 08-60-270-767-32-318 08-60-270-767-32-318 08-60-270-767-32-318 08-60-270-767-32-318 08-60-270-767-32-318 08-60-270-767-32-318 08-60-270-767-32-318 08-60-270-767-32-318 08-60-270-767-32-318 08-60-270-767-32-38-3 08-60-724-58-3-28-3 08-60-181-269-1173	PCT-US01-04098A-J554 PCT-US01-04098A-3522 PCT-US00-32990-19
Sequence 1677, Ap Sequence 1677, Ap Sequence 2094, Ap Sequence 12524, Ap Sequence 1522, Ap Sequence 1, Appli		Sequence 1554, Ap Sequence 3522, Ap Sequence 19, Appl

#### ALLONMENTS

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                                                                                                                                                                                                                                                                                                                                                                          AAB55834
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alteration in MMSC1 can be used to diagnose cancer. A germline alteration in an MMSC1 gene is indicative of a predisposition to cancer. A sometic mutation in an MMSC1 gene is indicative that the rissue is cancerous Analysis of MMAC1 and MMSC1 (or PDZ domain 6 of MMSC1) binding interactions can be used for detection of alterations in MMAC1 associated with cancer wild-type MMSC1 or a homologue can be used to supply wild-type MMSC1 gene function (or a substantially similar type MMSC1 gene function (or a substantially similar type MMSC1) which has lost the gene function due to a MMSC1 consentation for a cell, which has lost the gene function due to a MMSC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 these are used as immunogens for antibody production. Primers derived from MMSCl genomic clones can be used for identification of MMSCl genes and for synthesis by amplification of MMSCl PHA is PHA lettering an
                  23-NOV-2000
                                                              W0200069896-A2
                                                                                                                                                 allergy; asthma; multiple sclerosis; cancer; infection
                                                                                                                                                                        Hematopoietic cell; PD2; PL; autoimmune disease; inflammation;
                                                                                                                                                                                                                      PDZ encoded domain #4.
                                                                                                                                                                                                                                                              07-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                              AAB55834;
                                                                                                                                                                                                                                                                                                                                                   AAH55834 standard; Peptide; 344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1850 lavogetlegythegavailkhgrgtytltv 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1790 edtetppfklittlekgsejfyfsleggygeplydfptycktefalganaldychogdyl 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1730 ingqpldglehadrumlikmaggriilqvvadtmisalaaqlenmstqqhlgsptachhp 1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1675 rtwoinnelsdalgisiaggrgsplgdipv----fiamigasgvaartqklkugdrius 1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene mutation. The gene suppresses neoplastic growth of the cell.
Transgenic animals having an altered MMSCL can be used as a model for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a MMSC1 protein. The protein is a MMAC1 interacting protein which is involved in tunion suppression activity in the MMAC1 pathway. MMSC1, antiquals fragments or fusion proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Page 88-93; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MMSC1, an MMAC1 (tumour suppressor) interacting protein and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX86366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identifying drug candidates useful in treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 LSVNGVSVEGEHHEKAVELLKAAKDSVKLVV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 H-----PRVVELPKIDEGLGENVMGG----KEQNSPIYISPILEGGVAFPHGGIKPGDQL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 VNGCP------EFRARATAKATVAAFAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 RAIELLEKLOES------GEVFVHKLOSEKKVLOSEFCTALFEVYQYMHETIT //
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
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Best Local Similarity
Pakes 37; Censery
                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                 graff rejection, transplantation rejection), atheroscierosis, cancers, infectious discases, isohomia, vasulitis and Crohn's discase.
                                                                                                                                                                                                                                                                                                  colitis, ileitis, psoriasis, asthma, atopic darmatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                 a solid organ transplant. The method may also be used in the treatment of influenuation, allergy, influenuatory bowel discusses, ulcerative
                                                                                                                                                                                                                                                                                                                                                                  to treat a disease mediated by hematopoietic celis, e.g. autoimmune disease. It may also be used to prevent transplantation rejection of
                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a new mothod for modulating a biological function of an endothelial cell or hematopoietic cell. The method involves introducing into a cell, an antagonist that inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disciosure, Fage 28:43; 141pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bematopoletic cell, useful for freating autoimmune diseases and infectious diseases, by administering an antagonist that inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modulating a biological function of an endothelial cell or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lu PS;
                                                                                                                                                                                                                                                                                  insulin-dependent diabetes, Hashimoto thyroiditis, osieoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                     binding between a FDS protein and a PL protein. The inhibitor is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding between a PDZ protein and a PL protein
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14-FER-2000;
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                                                              166 EHHEKAVELLKAAKDSVKLVVRYTPKVL 193
316 asheqaalalknagqtvtilaqykpeti 343
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                                                                                                                                                                                                                 344 AA;
                                                                                                                                 Conservative
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2000US-0196527
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2000US • 0182296.
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99US-0134118.
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                                                                                                                                           15.5%, Soure 181.5, EB 2
42.0%; Pred. No. 9.3e-10;
                                                                                                                               19;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     skeletal muscle, in addition to lack of functional dystrophin, innow is normally targeted to the sarcolomma by associating to dystrophin (via the N-terminal PDZ domain (66 ad motif bearing homology to a he crogeneous ramily of signaling enzymes localised at cell-cell junctions) of inNOS, interacting Specifically with the PDZ domain of the alpha I syntrophin component). The binding proteins PSD 3 and -95 also have a PDZ domain and interact with nNOS mediating PDZ domain of the AbA NEWA receptor located at synapses the PSD proteins are involved in the development and involved involved in the developmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huntington's and Alzheimer's diseases and amyetropic lateral sclerosis), so inhibiting them (or their binding) can be used to treat atc. such diseases (associated with overactivation of HMDA receptors by excessive levels of nNoS. This method allows early diagnosis of MD. MD can now be treated by gene therapy, using only the fragment of dystropin involved in formation of the nNoS/sure lemma/dystraphin samples, rather than the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosing muscular dystrophy (MD) in a mammal by detecting absence or a decrease of neuronal nitric exide synthage (nHos) in a skel (a) mosale sample. Parieous with herbance or Beeker MD lock normal levels of nHos in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing muscular dystrophy by detecting absence or decrease of neuronal nitric oxide synthase (nNOS) in skeletal muscle sarcolemma using new nNOS binding post-synaptic density proteins, PS>-93 and need of the control of the cont
      W0200048002-A1
                                                                                                                                                                                                                       Human post-synaptic density protein 95 PSD95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page 74-76; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSD-95; also used for the diagnosis, prophylaxis and treatment of stroke and other neurodegenerative diseases
                                                                tomo sapiens.
                                                                                                                                                             Human: post-synaptic density protein 95; PSD-95; PDZ domain: GLGF loop;
                                                                                                                                                                                                                                                                                       21-FEB-2001 (tirst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      AAB22138 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete dystrophin gene which is too large to manipulate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT93775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 ATAKATVAAFAASEGHSHPEVVELPKIDEGLGENVIIGKEGNSPAYAGREITINGGVAERIKI 147
                                                                                                                              domain; muscular dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atrgpsvilgraistegeprksvilkystglytning; edgeningstilgggadisg 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATMICRIVED HITALIAN LANA TANDA LI LANA MERUTO (ANA ANTALIAN MENUNTA) I SALONA DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997-470555/43.
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                           20-JAN-1998;
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                                                                                            19-JAN-1999;
                                                                                                                                                      22-JUL-1999
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Query Match 16.6%; Score 194.5; DB 21; Best Local Similarity 41.4%; Pred. No. 1.5e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the protein sequence of the human post-synaptic density protein 95 (PSD-95). It is described with reference to the methods of the invention, which involve the identification of compounds
                                                                                                                                                                                                                                                                                                                                                                                 MMAC1 pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                 Human; MMSCl protein; MMACl interacting protein; tumour suppression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of the human MMSC1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY24025 standard; Protein; 1881 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-558226/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spillantini MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-2000; 2000WO-GB00374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to be disrupted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41% asheqaalalkmanjtrtilajykpos, siloakihali 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          767 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents tumour suppressor protoin NE-dly. The specification describes mammalian proteins, designated medasin, which bind to the tumour suppressor protein NE-dly. Nedasin is involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY30137;
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                                                                                                                                                                                                                                                              Human discs large 1 gene-2 cancer related molecule.
                                                                                                                                                                                                                                                                                                                                                                            15-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW48102 standard; Protein: 849 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 81-87; 104pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    formation of malignant tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUME ) SUMITIOMO BLECTRIC IND CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-AUG-1998;
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                                                                                                        internal secretion tissue.
                                                                                                                                                          Human: NE-dly, discs large I gene, cancer related molecule, merve,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 PEB 1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Hell | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 PRVVELPKTDFGLGENVMCGKEQNSETYTSETTPEGVAFFEGGLKEGTQLLSVNGVSVEG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 EHHFKAVFIIKAAKDSVKIVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 17.4%; Score 202.5; DB 20; Length 817; Local Similarity 43.4%; Pred. No. 2e-11; hes 43: Conservative 18; Mismatches 37; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents human dlg 2 molecule. The present invention describes human discs large i gene (dig family expressible in nerve tissue. Also described are: (1) a polymocleotide (PN) encoding dlg and comprising a 3100 (1) or 3213 bp (II) sequence; (2) RNA corresponding to PN having sequences (I) and (II); (3) RNA having a base sequence translated by dlg, (4) as antisces RN having a set least 15 bp sequence, and which is a part of PN of (1); (5) a derivative of the antisense PN; (b) an antibody specific for dlg, and (7) as antibody specific for a perpense. The polymoptide, RNA's and antibodies can be used for detection of dlg. The antisense PN can be used for detection of dlg. The antisense PN can be used as a thetapeutic composition for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSD 93, nNOS, neuronal nitric oxide synthase, Alrheimer's disease; diagnosis, muscular dystrophy, skeletal muscle, Huntington's disease; Duchenne muscular dystrophy; backer muscular dystrophin; sarectemmu, FTS domain; neurodegenerative disease; gene therapy;
                                                    08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amyotropic lateral sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Partial PSD-93 protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     composition(s) for treating cancer
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     proteins are involved in synapse formation by organising transmembrane neurorransmitter receptors through intracelular interactions. The inhibitors identified by the present lovention can be used to treat a disease mediated by haematopoletic cells, e.g. auroimmune disease, inflammation, allergy (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis, licitis, psoriusis, respiratory allergic diseases, (e.g. asthma), alopic dermatitis, autoimmune diseases (e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 - MAY - 1999;
14 - MAY - 1999;
14 - MAY - 1999;
21 - OCT - 1999;
                                                                                                                                                                                                                                 arthritis, multiple sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis, estemarthritis), atheroselerosis, cameens infectious diseases (e.g. viral intection), ischaemia, vasulitis and Crohm's disease. The inhibitors can also be used to provent transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 - OCT -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of proteins are named after three prototypical proteins: PSP95, brosophila large disc protein and Zonula eccindin 1 protein. PSZ domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for modulating a biological function of an endothelial cell or haematopoietic cell, comprises introducing into a cell an antagonist that inhibits binding between a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulating a biological function of a hematopoletic cell for treating an allergic response, or diseases mediated by immune system cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 JAN-2000; 2000US-0176195.
14 FEB-2000; 2000US-0182296.
11 APR-2000; 2000US-0196450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB58047
                                                                                                                                          Sequence
                                                                                                                                                                                                            rejection of a solid organ transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDZ domain protein and a PL domain protein to result in inhibition of leukocyte reliestion. The present sequence is a PDZ domain. PDZ domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure: Page 42; 143pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lax interaction protein 33 PG demain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       introducing into the cell a PDZ-PL interaction enlancer or -
                                                                                                                                          97 AA;
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9908-0162498.
9908-0176453.
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40.3%;
100.0%;
                                    Score 472;
   Pred. No. 1.8e-39;
                                    DB 22; Length 97;
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                                                                                                                                                              Query Match 17.4%; Score 203.5;
Best Local Similarity 43.4%; Pred. No. 2c-
                                                                                                                                                                                                                                                                                        the present sequence represents human dlq l molecule. The present invention describes human discs large 1 gene (dlq) family expressible in nerve tissue. Also described are: (l) a polynucleotide (PN) encoding dlq and comprising a 4100 (l) or 3215 bp (II) sequence: (2) kNA corresponding to PN having sequences (1) and (tl): (3) kNA having a base sequence translated by dlq. (4) at antiscuse PN having a at least 15 bp sequence, and which is a part of PN of (l): (5) a derivative of the antiscuse PN: (6) an antibody specific for dlq. and (7) an antibody specific for a polypertide having a 817 or 849 at sequence. The polypertide kNA's and antibodies can be used for detection of dlq. The antiscuse PN can be antibodies can be used for detection of dlq. The antiscuse PN can be
                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 14 16; 31pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    composition(s) for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human dions large 1 gene tamily
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; NE dlq; dises large ligene; cancer related molecule; nerve; internal secretion tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human discs large 1 gene-1 cancer related molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW48101;
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443 athequaaalkraqqsvtivaqyrpeeysiieskihdli 481
                                  16.6 KHRIDEAVELLEAAKISTVELVVSYTEKVIJILMSARFSKIJR 204
                                                                                                          194 - PHYSA PAACTTEM BESTEALVEGALENST ULJSNÖTSEGMAN (OTOTHEM BATTLAAN)
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                                                                       04 prkiilbkqstqlqtnipqq-osbositvstilaqqpadlsqeln.pdriispnapuln 442
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                                                                                                                                                                                                                                                                          therapeutic composition for treating cancer.
                                                                                                                                                                                                                                         817 AA:
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                                                                                                                                               ) Pred. No. 2e-1
18, Mismarches
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                                                                                                                                                                20-11:
                                                                                                                                                                                 Talk 19: Lamatta #17:
                                                                                                                                                 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases (e.g. rheumaloid arthritis, multiple sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis, grad fruit rejection, *ransplantation rejection) alberosclerosis, cred
                           transmembrane neurotransmitter receptor; autoimmune disease; transplantation rejection; inflammation; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 28-43; 141pp; English.
      inflammatory bowel discuse; alcerative
                                                                                                     PL domain protein; heukocyte activation; synapse formation;
                                                                                                                                    Endothelial cell; haematopoietic cell; PDZ domain protois;
                                                                                                                                                                                                      Tax interaction protein 33 PDZ domain.
                                                                                                                                                                                                                                                                                                                                                                                                         AAB57627 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infectious diseases, ischemia, vasulitis and Crohn's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ARBO-) ARBOR VITA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 VEGERHEKAVELLKAAKDSVKLVVRYTPKVLE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSHPRVVELPKTDFGLGENVMGGKEQNSFTYLSPLLPGGVAERHSGLKRODQLLSVNGVS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 2000US-0182296.
: 2000US-0186460.
: 2000US-0186527.
                                                                                                                                                                                                                                                                        (tirst entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.3%; Score 472; DB 22; 100.0%; Pred. No. 1.8e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
      colitis,
ileitis, psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Longth 97,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       inhibitors identified by the present invention can be used to treat a disease mediated by hashatopoletic cells, e.g. autoimmune disease, intlammation, allergy (e.g. drug allergies), inflammatory decesses, ulcerative colitis, ilelis, psoriusis, respiratory allergic diseases (e.g. asthma), atopic dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, maltiple selectosis, insulin dependent dialactes, Hashimoto
                                                                                                                                                                                                                                                                                              liseases (e.g. vital infection), ischaemia, asulitis and Crohm's disease. The inhibitors can also be used to prevent transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDZ domain protein and a PL domain protein to result in inhibition of kubwyte activation. The present acquares its a iDZ domain. PDZ domains of proteins are named after three prototypical proteins; PSD95, prosophila large disc protein and Zonula Occludin 1 protein. PDZ domain proteins are involved in synapse termation by organished transmembrane proteins are involved in synapse termation by organished transmembrane
                                                                                                                                                                                                                                        productive.
                                                                                                                                                                                                                                                                                                                                        thyroiditis, osteoarthritis), atheroselerosis, cancers, infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 30; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New inhibitors of binding of a PDZ protein and PL protein for inhibiting I cell-mediated response by hematopoietic cells, or for treating discuses characterized by inflammator, and humoral immune
                                                                                                                                                                                                                                                                                rejection of a solid organ transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurotransmitter receptors through intracellular interactions. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for modulating a biological function of an endothelial cell or hadmatopoietic cell, comprises introducing into a cell an antagonist that inhibits binding between a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    responses, e.q. inflammation, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WFI; 2001-025003,03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ARBO-) ARBOR VITA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ischaemia; vasulitis; Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    astima; atopic dermatitis; atherosclerosis; cancer; intectious disease;
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                      163 VEGEHHEKAVELLKAAKDSVKLVVRYTPKVLE 194
                                                                                               163 HSHPRAALIMUURUI MEMAMOGREÖNRAFIA ELIASILIM MANAHIMIN MUURIN 162
                                                        1 hahproolphtdeybeffsymyskepapiyiatlipgovaethajlkrądąlisymyzs 60
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                                                                                                                                         Conservative
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99US-0170453.
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                                                                                                                                                         100.0%;
                                                                                                                                                       40.3%; Score 472; DB 22; 100.0%; Pred. No. 1.8e-39;
                                                                                                                                         0; Mismatches
                                                                                                                                                                            Length 97;
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Rest Local Similarity 78.5
Matches 187: Conservative
31-MAR-1999; 990S-0127607;
e2-APR-1999; 990S-0127636;
u5-APR-1999; 990S-0127728;
30-MAR-2000; 2000US-0540763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        syndrome (AIDS), Addison's disease, altergies, anaemia, asthma, atheroselerosis, Crohn's disease, diabetes meditius, atopic dermatitis, glowerulonephritis, multiple selerosis, travo's disease, esteoarthritis, esteoporosis, psoriasis, rheumatoid arthritis, ulcerative colitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adrenoleukodystrophy, bown's syndrome, cystic fibrosis, Gaucher's disease, mysterie dystrophy, siekle cil adaemia, thaiaseachia, autoismune/inflammatory disorders such as acquired immune deficiency syndrome (AIDS), Addison's disease, allerques, anaemia, asthma,
                                                                                                                                                                                                                                                                                                                        cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; mataria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal bacmoglobhnuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                         anticonvolsant, osteopathic; ditiarthritie; immunosuppressant; cardiant; immunostimulant; thrombelytic; coamilat; creatrogle; antidibelic hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibaccerial; antitungal; actichoumatic; artibaccerial; antitungal; actichoumatic; dene therapy; cancer; proliferative disorder, hypoteosion; neurodespenerative disorder; osteoarthritis; graft vs host disease; antidocenterial; alternative disorder; hypoteosion; neurodespenerative disorder; osteoarthritis; graft vs host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipseriatic; antiparkinsonian, neotrapie, normalizationian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacterial, fundal, parasitic, protozoal and helminthic intections and cell proliterative disorders such as activity kerateris, actories between
                                                                                                              31-MAR-2000; 2000W0-US98621.
                                                                                                                                                           05 -acr-2000
                                                                                                                                                                                                      W1-200058473-A2
                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                         bone damage; cartilage damage; antlintlammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                          cardiovascular disease; diabetes mellitus; hypothyroidism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ORFX ORF3128 polypeptide sequence SEQ ID No:6256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB43364 Standard; Protein; 150 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and cancer including breast, bladder, bone marrow, brain and uterus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 MATLITVVQPLTLORDVAKAJELIEKI ÇEŞGEVEVHKI ÇSI KXVI ÇSBEÇIAJEKVYÇYMB 73
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                                                                                                                                                                                                                                                                                  contraceptive
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7815%; Prod. No. 2
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200-72;
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                                                                                                                                                                                                                                                                                                                                                                                            SCID; AIDS;
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Best Local Similarity 90.28;
Matches III, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antimpfinematory; antibucterial; antiviral; antimodal; antirhomatic; antithyroid; and antibucemic. The sequences can be used for determining the presence of or predisposition to or proventing or treating pathological conditions associated with an offex associated disorder. The matches can be used to express OFEX proteins in dence therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, esteoaithr tis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        North beliefs and poptibles defined from open realist frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                   ₩0200069896 A2
                                                                                                Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation: altery; asthma, multiple sclerosis, cancer; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacterial or fungal intection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage nocturnal haemoglobingia, autiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   graft vs host disease, cardiovascular disease, diabetes mellitus.
h,pertendide, h,pothproldism, chelesteral ester storage, systemic lupus erythemalesus, severe combined immunodeficiency (SCID), AIDS, viral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antipositatic, antiparkinsonian; mostropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaquisut; vasctropic
                                                                                                                                                             PDZ encoded domain #6
                                                                                                                                                                                                    07-MAR-2001
                                                                                                                                                                                                                                                AAH55836;
                                                                                                                                                                                                                                                                                       AAB55836 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coaquiation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antidiabetic; hypotensive, dermatological, immunosuppressive:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which represent the human oddX open reading frames i to 5161. The oddX sequences have activities such as eytostatic, bepatotropic, voluciary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG24446 to AAG27606 encode the proteins given in AAB40247 to AAB43337, which recressed the human oxiX open reading frames i to $161. The oxFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11: Page 5443; 5507pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                          139 qhq 141
                                                                                                                                                                                                                                                                                                                                                                                                                                 211 626 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 KATVAAFAASEGHSHPKVVELPKTUEGLGFNVMGGKEQNSPIYISEIIFGGVAERHGGLK 150
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are ascular for synthesising polynocloculdes, particularly full length cDNAs. The primers are also useful for the proteins encoded by detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cPNAs easily without any specialised methods. AARO3366 to AARO446 to AARO4833 represent human amino acid segrences; and AARO3465 to AARO3463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complementary strand of a polynucleotide which comprises a 5'-end sequence and an olidonucleotide comprising a sequence complementary to
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the 5602 nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dI primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesicing polymertectides, particularly the 5602 null-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligonucleutide comprises at least 15 nucleutides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of an oligonucleotide comprising a sequence complementary to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represent oligonucleot.des, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotide which comprises a 3' end sequence, where the
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Sugiyama T, Wakamatsu A, Wayai K, Otsuki
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                                                                                                                                                                                      69.6%; Score 8/4; DB 22; Length 197; 80.6%; Pred. No. 4.1e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Mismatches 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                 against intracellular parasites and also for diagnosis of disorders assectiated with expression of XMAD. They are also used for generating hybridisation probes useful in mapping the naturally occurring genomic sequences and to create knock in homologists, sinals (pigs) or transgenic animals (mice or rats) to model human diseases, oligonucleotide or longer fragments derived from the polynucleotide sequences may be used as elements on a microarray. Antibodies which specifically bind XMAD may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammator, disorder, acquired immane deliciency syndrome; AIDS; Addisor's disease; allerty; attachia; asthma; atheroselerosis; metanoma; Crohm's disease; diabetes mellitus; atopic dermatitis; lymphoma; concer; glomorulomophylis; multiple selerosis; former's disease; osteoarthritis; osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis; infection, cell proliticative disorder, actinic kitalosis, myeloma; arthritis; processes and college and college actinic kitalosis, myeloma; arthritis; processes and college actinic kitalosis; myeloma; arthritis; processes actinication and college actinic kitalosis; myeloma; arthritis; processes actinication and college actinication and college actinications.
XMAD, or in assays to monitor patients being treated with XMAD. D diagnosed, prevented or treated include genetic disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynomicotides encoding XMAD are useful in somatic or dermine denotherapy to correct a genetic deficiency, to express a conditionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               effectiveness as an agonist or antagonist of XMAD. The identified agonist of unlabilist are used for treating a discuss or condition associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 111-112; 135pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dese therapy; desette disorder; adrenoleukodystropby; leukaemia;
Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lethal dene product and to express a protein which affords protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with decreased or increased expression of functional XMAD. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adiesion molecule (XMAL), the XMAD is used for screening a compound for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a human extracellular matrix and cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymucleotide sequences encoding them, useful for diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human extracellular matrix and cell adhesion molecules and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baughn MR,
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                                                                                                  used for the diagnosis of disorders associated with the expression of
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In DAM, Shah P, Au-Young J;
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/note= "SH3 domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prevention and treatment of disorders associated with defective cell signalling. They may be used to treat curvers, neurological disorders and developmental disorders such as William's syndrome. CJPDZ or vectors containing CJPDZ may be administered to treat any of the above diseases by rectifying mutations or deletions in a patient's genome that affect cell signalling by expressing inactive proteins or to supplement the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid sequences in samples, and hence which patients may be in meed of restorative therapy. They may also be used to study the expression and tenefich of ourse projects demains and their role in collular sidualling the ourse projects defaults may be used to antiacus in the production of antibodies and in assays to identify medulators
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cell junction PDZ protein; CJPDZ; antiqen; antibody; cytostatic; anti-leukaemic; neuroprotective; anticplieptic; anti-Alzheimer's diseas nootropic; anti-convulsant; cancer; leukaemia; myeloma; sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell signalling by expressing inactive proteins or to supplement the patients own production of CJPDZ protein domains. Antisense nucleic acid molecules may be administered to down regulate CJPDZ protein domain expression by binding with the cells own CJPDZ genes and preventing their expression. CJPDZ polynucleotides may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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24 - Jul. - 2001
                                                                        ris6265547-B1
                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    neurological disorder; epilepsy; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cell junction P57 protein CIPI/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-407-2001 (tirst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU07127 standard; Protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of CJPD2 expression and activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CJPD2 polymuclectides and proteins may be used in the diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents human cell junction PDZ protein (CJPDZ).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 AA;
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107..189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB93600 standard; Protein; 197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 control/regulate expression and activity of CIPDZ. The anti-CIPDZ antibodies may also be used as diagnostic agents for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide. The polypeptide may be used as an antiquo in the production of antibodies against CJFD2 and in assays to identity molecules which bind till be including modulators of CJFD2 expression and activity. The anti-CJFD2 antibodies, agonists and antagonists may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1; 28pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cellular junction PDZ proteins useful in the prevention, diagnosis and treatment of disorders associated with defective cell signalling such as
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Human; primer; detection; diagnosis; antisense therapy; wene therapy
                                                                                                                           Human protein sequence SEQ ID NO:13638
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result.	Score	Query Match	Query Match Length DB	H	0.1	Description
- 1	1170	100.0	233	20	AAY29978	Human cell junctio
2	1170	100.0	233	6.2 6.2	AAU07127	Haman cell junctio
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Q18165;
InterPro: IPR000619: Gaanylate_kin.
InterPro: IPR001478; PDZ:
InterPro: IPR001478; SH3.
Plam: PF00625; Guanylate_kin; L.
Plam: PF00595; PDZ; 4.
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Bukaryota: Metazoa: Mematoda: Chromadoro.
Khabditidae: Peloderinae: Caenorhabditis.
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01-JUN-2001 (TrEMBLrel 17, Last sequence update)
01-JUN-2001 (TrEMBLrel 17, Last annotation update)
                                                                            EMBL; U39742; AAK39197.1;
HSSP; Q12959; 1PDR.
                                                                                                                         STRAIN BRISIOL N2; Waterston R.;
                                                                                                                                                                                   "The sequence of C. elegans cosmid C25F6."; Submitted (NOV-1995) to the EMBL/Genbank/DDBJ databases
                                                                                                                                                                                                                      Bentley D.;
                                                                                                                                                                                                                                   STRAIN BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                           STRAIN BRISTOL N2; MEDLINE 99069613; PubMod=9851916;
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SPQUENCE 967 AA: ID644] MW: 4400011405656563 (16954)
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NCBI_TaxID-6239;
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                                                                                                                                                                                                                                                                                                              "Genome sequence of the mematode C. elegans: a platform for
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Best Local Similarity
Matches 48, Conserv
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SMART: SM00072; GuKc; 1.
SMART: SM00228; PDZ; 3.
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48.5%; Pred. No. 1.
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01-JAN-1998 (Fremkirel 05, Last sequence update)
01-JAN-1998 (Fremkirel 17, Last sequence update)
01-JIN-2003 (Fremkirel 17, Last sequence update)
01-JIN-2003 (Fremkirel 17, Last sequence update)
HYPOIHELICAL 19.0 KDA PROTEIN (FRAAMENI).
8chistosoma mansoci (Blood flake)
Eukaryota, Metazoar Platybolmininthes; Rhabditophora; Neodermata;
Fremkirola; Diqenea; Strippidida, Schistosomatoider; Schistosomatidae;
lgterPro: [PR001478; PDZ
PLAM; PF00595; PDZ; ],
SMART: SM00228; PDZ; ].
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01-MAY 2000 (TrEMBLIEL 13, Last sequence update)
01-JUN-2001 (TrEMBLIEL 17, Last annotation update)
Y54G11A.10 PROTEIN.
Y54G11A.10.
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Submitted (cOTT-1997) to the PMRL/Content/Johns
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EMBL: AL034488: CAA22459.1:
HSSP: Q12959: 1PDR.
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SEQUENCE 317 AA: 35762 MW: 7788850898735889 CRC64;
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SMART; SM00228; PDZ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wallis J.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 TARRRQOQQL 214
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                                                                             Q9B179
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                                                                                                              RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 55.0%; Score 644.5; DH 5; Lenath 297; Best Local Similarity 70.6%; Pred. No. 1.6e-41; Matches 127; Conservative 29; Mismatches 23; Endel: 1
Q9B175;
Q9B179;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
LIN 7 (FRAGMERT).
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NON_TER 297 297
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Piam; PF00595; PDZ; 1.
SMART; SM06228, FDZ; 1.
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Simske J.S., Kaech S.M., Harp S.A., Kim
"LET 24 receptor localization by the ec
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01-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                            237 HEBSIKESINGLIANNE NULAH HIHIH HEBIN NESANGSANGKALAH HIHIH HIH HIH HIH HIH HIHI
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                                                                                                                                                                                                                                                                                                       117 TERROQUETERMENVERTGEVNAKLASEQQVEQSECTEAVREVVETVVERTOADTIEGT 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 LIMEVARALELLERIWESCEALARHOSTERATÖSEEGTVINGARATOTANGALEL 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 EVEVEROUPERE LEAGUE OF THAT HAVE LEVEL THE THAT BANGLAND AND AND THE THE TOTAL
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                                        FRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33580 MW; ABF15EDB90B0A90E ('Kr'64;
                                                                                                                                                                                                                                                              $XI:
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RESHLT 10

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Best Local Similarity 98.7
Matches 149; Conservative
                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Pterydota: Neoptera: Endopterydota: Diptera: Hrachycera: Muscomorpha:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TEEMBLECT 10, 01-MAY-1999 (TEEMBLECT 10, 01-JUN 2001 (TEEMBLECT 17,
MEDI INF-20196006; PubMed 10731132;
                                                                                                                                          VELL OR CG7662.
                                                                                                                                                        CG7662
                                                                                                                                                                   09VBY7;
01-MAY 2000 (TrEMBLrel, 13, Greated)
01-JUN-2000 (TrEMBLrel, 13, Last annotation update)
                                                                                                                                                                                                                                  Q9VBY7
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SMART: SM00228, FD2; 1
PEGS17E; PS50107, FD2;
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EMBL: AF090134; AAC78073.1; -.
HSSP: U12923; 3PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation and Characterization of Mammalian Homologues of Caenorhabditis elegans lin-7. Localization at Gell Geti Junetion.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9Z251;
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                STRAIN BERKELEY;
                              SEQUENCE FROM N.A.
                                                           NCB1_Tax1D-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Trie M., Hata Y., Deguebi M., Ide M., Hirac K., Yao I., Mishloka H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia: Eutheria; Redentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus morvegious (Rat).
                                                                         Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 ISRIIFGGVAEPHOGLKPODQLLSVNGVSVF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 EEMEARFEKLETARRE 209
                                                                                                                                                                                                                                                                                                                                                                  14 MATIJVVQPIJILDRDVARATRITEKIQESGEVPVHKIQSLKKVIQSSRVIAIREVVQVMH 73
                                                                                                                                                                                                                                                                                                        ISRIIPGGVAFRHGGLK.GDQLLSVNGVALF [5]
                                                                                                                                                                                                                                                                                                                                                                                                                              MATLITYVQPIJILDPDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMH 60
                                                                                                                                                        PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 AA: 19927 MW; D448E3BBCF5A51DB CRC64:
                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVNIWI LAND
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98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 758, DB 11, Pred. No. 1.6e-50;
                                                                                                                                                                                                                                PKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 AA
                                                                                                                                                                                                                                195 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 182
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RA Hallow R.M., Basen D., Baxendalle J., Hayraktaroqin L., Bedakey E.M.,

RA Horkova D., Botchan M.R., Houck J., Hrokstein P., Brottier P.,

RA Hurtls K.C., Botchan M.R., Houck J., Hrokstein P., Rrottier P.,

RA Hurtls K.C., Busam D.A., Buffer H., Cadieu E., Center A., Chandra I.,

RA Graben E., Dearley S., Dabike C., Bavenport L.B., Davies P.,

RA Graben E., Erigh L.E., Downes M., Degan-Rocka S., Bunkey B.C., Dunn P.,

RA Foster C., Cabrielian A.E., Garq R.S., Gelbart W.M., Glassor K.,

Padison K., Evarpetista C.C., Ferrac C., Ferrica S., Fletschmann W.,

RA Graben A., Pag E., Garge I., H.S., Gelbart W.M., Glassor K.,

PA Graben A., Pag E., Garge I., H., So F., Carle E., Harris M.,

RA Hostin D., Houston K.A., Howland T.J., Branchen J.A., Kolohum K.A.,

RA Kiamel B.E., Kodieu C.D., Kraft C., Krevita S., Kulp D., Lai Z.,

RA Kiamel B.E., Kodieu C.D., Kraft C., Krevita S., Kulp D., Lai Z.,

RA Malson D.H., Nelson K.A., Nixon K., Nusskern D.K., Pacleb J.M.,

RA Markilov G., Milshina N.J., Moarry C., Morris J., Moshreli A.,

RA Keinert K., Spradling A.C., Simpson M., Skopski M.P., Smith T.,

RA Spier E., Spradling A.C., Simpson M., Skopski M.P., Smith T.,

RA Williams S.M., Mooddag T., Wolfrey K.C., W D., Yang S., Yao Q.A.,

RA Williams S.M., Mooddag T., Wolfrey K.C., W D., Yang S., Yao Q.A.,

RA Williams S.M., Mooddag T., Wolfrey K.C., W D., Yang S., Yao Q.A.,

RA Kinder S.M., Wooddag T., Wolfrey K.C., W D., Yang S., Yao Q.A.,

RA Kinder S.M., Wooddag T., Wolfrey K.C., W D., Yang S., Yao Q.A.,

RA Kinder S.M., Wooddag T., Wolfrey K.C., W D., Yang S., Yao Q.A.,

RA Kinder S.M., Wooddag T., Wolfrey K.C., W D., Yang S., Sheel L.,

RA Kinder S.M., Wooddag T., Wolfrey K.C., W D., Yang S., Sheel L.,

RA Kinder S.M., Wooddag T., Wolfrey K.C., W D., Yang S., Sheel L.,

RA Kinder S.M., Wooddag T., Wolfrey K.C., W D., Yang S., Sheel R.,

RA Kinder S.M., Wooddag T., Wolfrey K.C., W D., Yang S., Yao Q.A.,

RA Kinder S.M., Wooddag T., Wolfrey K.C., W D., Yang
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Bost Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 148, Conservative 20, Mismatches 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M.D. Celniker S.E. Holt R.A. Evans C.A. Godayno J.D., Amanda Hes P.G. Sherer S.E. Li F.W. Baskins R.A., Calle R.F., George R.A. Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton C.C. Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Frandon R.C., Royers Y.-H.C., Blazej R.G., Champe M., Pteiffer B.D., Wan K.C., Edges P. Baxter E.G., Het J., Welson C.K., Miklos G.L.G., Rein J. R., Dayle S., Baxter E.G., Het J., Welson C.K., Miklos G.L.G., Rein J. R., Bayle S., Baxter E.G., Het J., Welson C.K., Miklos G.L.G., Rein J. R., Bayle S., Baxter E.G., Het J., Welson C.K., Miklos G.L.G., Rein J. R., Bayle S., Bayter E.G., Het J., Welson C.K., Miklos G.L.G., Rein J. R., Bayle S., Bayter E.G., Het J., Welson C.K., Miklos G.L.G., Rein J. R., Bayle S., Bayter E.G., Het J., Welson C.K., Miklos G.L.G., Rein J. R., Bayle S., Bayter E.G., Het J., Welson C.K., Miklos G.L.G., Rein J. R., Bayle S., Bayter E.G., Het J., Welson C.K., Miklos G.L.G., Rein J., Rein J., Bayter E.G., Het J., Welson C.K., Miklos G.L.G., Rein J., Rein J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PS50106; PDZ;
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186 DKQRNTBRBQ 195
                                                                                                                      201 EKIRIARREQ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 CPEFFARATAKATVAAFAASEGHSHPRVVELPKTIEEGLGENVMGGKEQNSPTYTSRTTPG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 SHDVKASATAKATVAAFAASEGHAHPRVVELPKTEEGLGENVMGGKEQNSPIYISRIIPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 EFFLILSREVARKS (ELLEKLIANSIDE PELIKLIAN), DIVINSIDEM I SVRBVVEHVVETVOTIGG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Agbayani A., An H. J., Andrews Pfannkoch C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21493 MW; EF9DF5ED71A73FBC CEC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.4%, Score 754, DB 5, 77 9%; Pred No 3 5e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                             Query Match
Best Local Similarity
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Hest Local Similarity 79.2%; Pred. No. 2.4e-54;
Matches 157; Conservative 24; Mismatches 15; Indels
                                                                        Mat Ches
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE KIDNEY;
Olsen O., Liu H., Merot J., Welling P.A.;
"Basolateral Membrane Expression of the Kir 2.3 Channel is Coordinated by a FDZ Interaction with Lin-72/2ASK.";
Submitted (oct-2000) to the FMED/GenEack/EdFC databases.
BMBD, AF311862; AAG34117.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAP-2001 (TrEMBLrel, 16, Created)
01-MAR-2001 (TrEMBLrel, 16, Last sequence update)
01-JUN-2001 (TrEMBLrel, 17, Last accetation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9HAP6
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Jo K., Derin R., Li M., Bredt D.S.,
"Characterisation of MAIS/Velia 1
                                                                                                                                                                                                                                                                                                PIAM: PF00595; PDZ; 1.
SMART; SM00228; PDZ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota: Matazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Neurosci, 19:4189-4199(1999),
EMBI: AF087604: AAC78482.1,
EMBI: AF173082: AAD48501.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 EFMEAPFFKMRSARREQQ 196
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                                                                        157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q12923: 3PDZ
                                                                                                                                                                                                                                        207 AA;
                                                                     Conservation
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                                                                                                                                                                                                                                     22896 MW; 63189D82706B9H00 CRC64;
                                                                                                 69.0%; Score 807; DR 4.78.5%; Pred. No. 3.4e-54;
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Query Match

Local Similarity 79.1 hes 155; Conservative

68.3%; Score 799; 79.1%; Pred. No.

8; Score 7'9; DB 11; Length 2'4; 8; Fred. No. 1.6e-53; 24; Mismatches 15; Indels 2

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RA Arakiwi T., Hara A., Pikraiski Y., Kince H., Adachi J., Erakuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Gkazaki Y., Gojdbori T., Romo H., Kasukawa T., Saito R.,
RA Radota K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Radota K., Matsuda H.A., Ashburner M., Betaloy S., Gusawant T.,
RA Radota K., Matsuda H.A., Ashburner M., Betaloy S., Gusawant T.,
RA Robell P., Iowis S., Matsud Y., Nikaido I., Posole G., unackedush J.,
RA Kushi P., Iowis S., Matsud Y., Nikaido I., Posole G., unackedush J.,
RA Kushi I., Matsud Y., Nikaido I., Posole G., unackedush J.,
RA Kushi R., Okido T., Furunno M., Annida M., Washino I., Kashi O.,
RA Sakai K., Okido T., Furunno M., Carninci P., de Bohaldo M.F.,
RA Biowistein M.J., Balt C., Fietcher C., Fritta M., Gariboldi M.,
RA Kushi K., Okido T., Furunno M., Hume D.A., Kaniya M., Iace N.H.,
RA Gustincich S., Hill D., Holmann M., Hume D.A., Kaniya M., Iace N.H.,
RA Lyons P., Murchichi L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Fing B., Ringwald M., Redriquez I., Sakamoto N.,
RA Sasaki H., Gato R., Sheebenh C., Saya T., Sibata Y., Sakai K.,
RA Nordone P., Fing R., Ringwald M., Redriquez I., Sakamoto N.,
RA Sasaki H., Gato R., Sheebenh C., Saya T., Sheata Y., Stataki S.,
PA Nordone P., Fing R., Ringwald M., Redriquez I., Sakamoto N.,
RA Sasaki H., Gato R., Sakai K., Wanta K.H., Welto G., Wilttaker C., Wilming I.,
PA Nordone P., Sakai K., Wanta K.H., Welto G., Wilttaker C., Wilming I.,
PA Nordone P., Sakai K., Wanta K.H., Welto G., Kiltaker C., Wilming I.,
PA Nordone P., Sakai K., Wanta K.H., Welto G., Kiltaker C., Wilming I.,
PA Nordone P., Sakai K., Wanta K.H., Welto G., Kiltaker C., Wilming I.,
PA Nordone P., Sakai K., Wanta K.H., Welto G., Kiltaker C., Wilming I.,
PA Nordone P., Sakai K., Wanta K.H., Welto G., Kiltaker C., Wilming I.,
PA Nordone P., Sakai K., Wanta K.H., Welto G., Kiltaker C., Wilming I.,
PA Nordone P., Sakai K., Wanta K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09D201:
01-JHN 2001 (IrEMBL:el. 17, Greated)
01 JHN 2001 (IrEMBL:el. 17, Last sequence update)
01 JHN 2001 (TrEMBL:el. 17, Last annotation update)
VERTERRATE HOMOLOG OF C. ELECANS LIN-7 TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECURATE FROM R.A.
STRAIN C57BL/6J; TISSUE-HIPFOCAMPUS;
MEDILME-21085660; Fubmed-11217881;
                                                                       Pfam; PF00595; PDZ; 1.
SMARI; SM00228; PDZ; 1.
FR0511E, PSC0106, FEZ;
                                                                                                                                                                                                                                                                                                                                                                             EMBL: AK019299; BAB31655.1; MGD; MGI:1330858; Veli2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB:_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus muscalus (Mouse).
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                                                                                                                                                                                                                                                                                                             InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
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| TELETITITE FELLET TELETITITET TELETITET TELETITET TELETITET TELETITET TELETITET TELETITET TELETITET TELETITE
| TELETITET TANKER OF TAKEN TELETITET TELETITET TELETITET TELETITET TELETITET TELETITET TELETITET TELETITET TE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTI ATASHATKASAMAACUZGATKAPONANAUPRICARVI ATATHATTI TI 1 1 11 6.5
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234 AA; 25732 MW; 7691908B1029E53B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 63.6%; Score 814; DR Host Local Similarity 80.6%; Pred. No. 9.3e; Matches 154; Conservatize 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES Monse;
MEDLINE 99274724; PhbMcd 1034122;;
Jo K. Derin R., Li M., Bredt D.S.;
"Sbaratterization of MALS; Volta";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and Characterization of Mammalian Romatogues of Caenorhabditis elegans lin-7: Localization at Cell-Cell Junetion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A tripartite protein complex with the potential to couple synaptic vesicle exocytosis to cell adhesion in brain."; cell 94:773-782(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.": Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES Mouse: STRAIN C57HL/61: T19SHF TESTIS; MEDLINE 21085660: PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIN-7 homologs enriched at brain synapses in association with the postsynaptic density-95/NMDA receptor postsynaptic complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ptam; PF00595; PDZ; 1.
SMARI; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES - Rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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126 STADRIBOTKIONAL SVINOVSVIDTHIBKAVINTIKAAQGKVK: VVFVTEKVILITHITTITT 185
                                                                                                                                                                                                                       81 CPEFRARATAKAFVAAFAASECHSHPRVVELPKTUEGLGENVMCCKEGNSPIYISRIIPG 140
                                                                                                                                                                                                                                                                                                                                                               21 QPUTIDKDVAKATELLEKIJESGEVPVHKLÖSIKKVIJSEFCTATKEVYÖYMHETTIVNG 80
                                                                       CVABRHOOLKENE, LLSVNSVSVENEHBEFAVET FAAFESVET VVEVTEFVLEDMFASE 200
                                                                                                                                               SPEVRANATAKATVAAFAASEGHSHPRVVELPKTEEGLGFNIMGGKEQNSPIYISRIIPG
                                                                                                                                                                                                                                                                                       EPVKLERDICRAIHLLEKIGESSEVEPQELQALGEVIGSEFCHAVREVVEHVYETVDISS 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF087695: AAC78483.1: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50106; PDZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.6%; Score 814; DB 11;
B0.6%; Pred. No. 9.30 55;
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    and the tending or commutation

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14 I., Fakuda !
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Best Local
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01-JUN-2001 (TrEMBLIEEL 09, Last sequence update)
001-JUN-2001 (TrEMBLIEEL 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Intellio, IROS95, PDE: 1.
ENANG, PROSEDS, PDE: 1.
EMARG, SMOGELS, FDE: 1.
PROSEUR: PSS0106; PDE: 1.
SEQUENCE 207 AA; 22900 MW; BC6H6754BBC89B14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q98252;
Q98252;
Butz S., Okamoto M., Sudhot T.C.;
"A tripartite protein complex with the potential to example symaptor
vestele exceptosis to cell adhesion in brain.";
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Mammalia; Butheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                            NCB1_Tax1D=10090;
                                                                                                                                                                                           Mus musculus (Mouse)
Eukaryota: Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                    088951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF090133; AAC78072.1; -. HESP: Q12923; Prof.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation and Characterization of Mammalian Homologues of 
Cuenoriabilitis elegans lin 7. Localization at Cell-Cell Junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCB1_TaxID=10116;
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             VELIZ OR MALS-2
                                                                                                                                                                                                                                                                                                                                                                088951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oncodene 0:0-0(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Irio M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEÇUCATO PROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIN-7-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 REMEAREEKMRSARRROG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 EKMRSAKRKOQ 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 SEMEARSEKLESARERQQ 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 MATETYVÕH TEDROVARATELEKTÕPSCHVEVHKTÕSLKKVLÕSEROTA-REVVÕYMH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 DILIDITGSAFVKAHATAKATVAAFTASEGHAHPPVVELPKTDEGLGENIMPRKEQNSPIY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 TO CONSOLUTERARALANATANATAASEEHSHERVVETERNIDESTEENVMOTNEONSELL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAAL VEEKSE PERVERANTS PELOPS TO PROPERTY OF THE HIGH HITCH SEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cal Similarity
157; Comserv
                                                                      NE 98101016, EubMed 9759324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISKVIPGGVAHRHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAQGSVKLVVRYTPRVL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., Hata Y., begwehi M., Ide M., Hirae K.,
                                                                                                                                                                       Eutheria; Rodentia; Sciuroqnathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRISTIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 2.4e-54;
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Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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InterPro: 1PR001478: PDV
P1am: PF00595; PDZ: 1.
EMART: ЧМ00228: PDC: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS50106; PDZ;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinac; Kattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegious (Rat).
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121 NAMOGKEÖNSETATERGAARERHOSI KEGIÖTTERAAAREHEKAARTIKVAVKE 180
                                                                                                                                                                                                                                                               61 ETTIVNGCPFFRARATAKATVAAFAASHOHSHPFVVELPKIDEGIGENVMGGKEGNSPTY 120
                                                                                                                                                                                                                                                                                                                              74 ETTTVNGOPEPBARATAKATVAAFAASECIISHEEVVETER DECLOEMVAGERQASDIY 133
                                                                                                                                                                                                                                                                                                                                                                                                                               | 14 MATLIVVQPL/TLDH/DVARAJEL/FKI/PS/CEVPVHKI/PSI/KKVI/PSF/CTAJPSVVYVMH-73
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                                                                                                                             ISKLIPGGVAERHOOLKROOM I SVNOVSVEJERREKAVELLKAAROSVKLVVKYLEKVL. 193
                                                                                                                                                                                                                                                                                                     233 AA; 25997 MW; D8D05EF16A93BE7B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.1%; Score 1077.5; DB 98.6%; Pred. No. 8.3e-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24544 MW; FIREAANINGOTINGA CINA (
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01-001-2000 (TERMHITCH, 15, Last sequence update)
01-011W-2001 (TERMHITCH, 17, Last annotation update)
crwa Fillin's Fis. Crewn Fiactionaddo, wearly Similar in Channel
SEQUENCE FROM N.A.

SPECIES-MOUSC: TISSUE-HEART;

SPECIES-MOUSC: TISSUE-HEART;

MEDLINE-98424246: PubMed 9753424;

Bulz S., Okamoto M., Sudhot T.C.;
                                                                                                                                                                                                                                       Eukaryota: Metazoa; Chórdata: Craniata; Vertebrata; Enteleostos.);
Maamalia, Entheria, Rodeatia, Aliuroquathi; Muridae: Murinae; Mus
NCBI_TaxID-10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse), and
Rattus pervedicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VELLY OR MALS-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1999 (TrEMBLIEL 09, Last sequence update)
01-JUN-2901 (TrEMBLIEL 17, Last annotation update
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EMBL, AK002077; BAA92072.1;
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Ninomiya K., Iwayanagi T.,
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Eukaryota, Metazoa, Chordata, Graniata, Vertebrata, Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASSOCIATED PROTEIN OF SYNAPSE-110.
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1: sp_archea:*

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14: sp_unclass
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Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMAR1ES

Result	Score	Query Match	Query Match Length DB	#	ID	Description
	1170	100.0	233	إحد	014910	014910 homo sapien
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_	814	69.5	197	4-	©9NUP9	Q9nup9 homo sapien
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J	809	69.1	207		C92252	Q9=252 rattus sorv
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1 ,	643.5	55.0	297	, n	P90976	F90976 caenorhabdi
14	244.5	20.0	967	٦	Q9B179	©9bi79 caenorhabdi
15	234.5	20.0	1064	Un	Q18165	Q18165 caenorhabdi
<del>-</del>	208.5	17. x	960	ຼາ	Q9VYZ5	Q9vyz5 drosophila
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n I	198.5	17.0	4.5E	4.	Q9HD26	g9hd26 homo sapien
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HIBELER 92277224 Paber 10341223;  HIBELER 92277224 Paber 10341223;  Jo K., Berlin K., Li M., Brodt D.S.;  "Narawiterination of MALS/Velia L. 2, and one a family of mammalian IIII-7 homologs enriched at brain synapses in association with the posts, agric 5 as 1, 20 A199 (1292).  EMBL AMSST633 AAC78481.1; s. EMBL AMSST633 AAC7848500.1; s. EMBLE AMSST633 AAC78	SEQUENCE FROM N.A.  FISSUE TESTIS; Published 9753324; HHDLINE 98424216, PubMed 9753324; HHDLINE 98424216, PubMed 9753324; HHLL S., okameto M., Sudhof T.C.; "A tripartite protein complex with the potential to couple synaptic vesicle exceyrosis to cell adhesion in brain."; cell 94:773-782(1998). [2] [2] SEQUENCE OF 32:233 FROM N.A. ROUSSET R., Fabre S., Dasbois C., Bantiquies F., Jalinot P.; cencere 15:0-9(1997).	O14910 PRELIMINARY; PRT; 233 AA. O14910; PRT: 233 AA. O14910; O1-JAN-1998 (TrEMBLICEL 05, Created) O1-JAN-1998 (TrEMBLICEL 17, Last annotation update) O1-JUN-2001 (TrEMBLICEL 17, Last annotation update) O1-JUN-2001 (TREMBLICEL 17, Last annotation update) VELL 1 (TAX INTERACTION PROTEIN 33) (FRAMMENT). Homo sapiens (Human). BEAKATYOTA: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi; Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo. NCHI_Taxin-9606;

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Title:
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hypothetival prote	2 T00346	1281	12.4	144.5	Ξ
tyrosine kinase ac	601158	450	12.4	144.5	40
eye development pa	A56158	1893	12.4	145.5	ã
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# ALIGNMENIS

RESULI

hypothetical protein TS4G11A.19—Caemorbab-litis elegans C)Species: Caemorbabdicis elegans C)Stecies: 15-0ct-1949 #sequemec\_revision 15-0ct-1949 #text change 15-0ct loop C)Accession: T27179 R)Wallis, J.

Submitted to the EMBL Data Library, December 1998 A;Reference comber: 223922 A;Reference comber: 223922 A;Reference comber: 127179 A;Reference comber: 127179 A;References: DNA A;Residues: 1-317 < VMLL A;Residues: 1-317 < VMLL A;Residues: 1-317 < VMLL A;Reperimental source: clone y54011A C;Genelies: A;Gene: CESP:Y54011A.10 A;Ratches: 130; Conservative
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C;Species: Homo sapiens (man)
C;Date: 21-Dec 1996 #sequence
C;Accession: G01974
A;Reference number: G08966
A;Accession: G01974
A;Status: preliminary; translated from GR/EMPL/DDBJ
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channel associated protein of synapse - human
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E:198-276 [Pomain: GIGF demains herelagy -gIGP
E:543-501/Pomain: SH3 ham-lagy -SH3
E:663-840/Demain: gnanylaro kinase bemelagy -gKTS
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C:Species: Buttus nerrogicus (Norway rat)
C:Date: [6-Jul-1999 #sequence_revision | 16-Jul-1999 #fext_change 21-Jan-2000
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A;Molecule type: DNA
A;Residues: 1-1131 <BEN>
A;Cene+ferences: EMBL:U39742; NIP:g1049455, PID:g1049456; PIDN:AAA80434.1; CESF:C25F6
C;Gene+fes;
A;Gene+fesp:c25F6.2
A;Introns: 16571, 21675, [REN], REN], A; L. A; C; A; C; C; C; L. B; C;
                                                                                                                                               submitted to the EMBL Data Library, July 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Irie, M.; Hata, Y.; Takai, Y.
submitted to the EMBL Data Library, April 1996
A:Description: Cloning of new isoforms of PSD-95/SAP90 related genes
A:Reference number: 217166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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35.7%, Pred. No. 1.1e-08;
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A;Gene: chapsyn-110
C;Superfamily: dises large tumor suppressor: GLGF domain homology: guanylate kinase h
E,199 (2), Johnson: JETH disentional rolly officer
F;543-601/Domain: SH3 homology (SH3)
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Arketerence number, Assest, Mülbisissus94
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C:Species: Drosophila melanogaster
C:Dato: | U SCP: 1999 #sequence_revision lu Sep:1999 #text_change lu Sep-1999
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E:771-948/Besain. juanylate kinase homology (SK)
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A; Residues: 1 960 WO
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A:Residues. 1 870 kKTMs
A:Closs references RMP
C:Genetics:
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C;Superfamily: discs-large tumor suppressor,
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F:159-241/Domain: GLGF domain homology <6162>
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Best Local Similarity 39.3%;
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Best Local Similarity
525 ELEPGYGIUSVNNVNLTHATHEEAAQALKTSGGVVTLLAQYEPEBYNFFEAFIQELK 581
                                                                                            148 GLKEGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVEYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                              THE AVERSTEADSTRUTTED HER CONTINUED TO THE TENTON STATES SOME
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29.3%; Pred. No. 1.5e-08;
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39.3%; Pred. No. 8e-08;
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A:cross-retorences: GB:M96853; NID:g206454; PIDN:AAAA1971.1; PID:g206455
A:Experimental source; brain
C:Superiamily: discs-large rumor suppressor: CICF demain homology rangulate kinase bome
F:70-148/Remain: CICF demain homology rGLG1:
F:165-243/Remain: GICF demain homology rGLG2:
F:443/Remain: GICF demain homology rGLG2:
F:4435-4943/Remain: GICF demains SHI homology rGLG2:
F:4435-4943/Remain: GICF demains SHI homology rGLG2:
F:445-4943/Remain: GICF demains SHI homology rGLG2:
F:445-4943/Remain: GICF demains SHI homology rGLG2:
F:4535-712/Remain: GICF demains SHI homology rGLG2:
F:5435-712/Remain: GICF demains SHI homology rGLG2:
F:5435-712/Remain: GICF demain homology rGLG2:
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Allith: SANO, a rat presynaptic protein related to the produc of the Drosophila tumo ArRetorence number: A45436; MUTE-CALRETAU
ArActession: A45436
ArStatus: proliminary not compared with exaceptual translation
ArMeteorior type: notice acid
ArResidues: 1-729 ZKIS:
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A:Molecule type: mkNA
A:Residues: 1-724 <CHO>
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A:Note: sequence extracted from NCBI backbone (NCBIP:126555)
C:Superfamily: discs-large tumor supercasor: GLSF domain homology, quanylate kinase home
E:70-1487/omain: SLEE domain homology: SLEE.
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C/Species: Rattus more-gious (Norway rat)
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Neuron 9, 929-942, 1992
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E:435-493.799mile: SP3 bymylegy <9H35
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                                                                                                                                                         370 ASHFQAATALKNAQQTVTLTAQYKPEEYSEFEAKTHDLK 408
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41.4%; Pred. No. 4.5e-07;
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41.4%; Pred. No. 4.5e-97;
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Aldene: PSD95
C)Supertamily: discs-large tumor suppressor: GLGF domain bomology: quanylate kinase h [5]Supertamily: discs-large tumor suppressor: GLGF domain bomology: quanylate kinase h [5]SE5-286/Domain: SH3 homology: SH3  
[7]SE5-286/Domain: SH3 homology: SH3  
[7]SE5-286/Domain: quanylate kinase hadalid; -3E1-
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C:Superfumily; discs large tumor suppressor; GLGF domain homology; quanylate kinase h
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Proc. Natl. Acad. Sci. U.S.A. 91, 9818 9822, 1994
A:Title: Clouing and characterization of halg: the human homologue of the Drosophila
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C.Fate. (1 Mar 1996 Asequence_recision 01 Mar 1996 (text_change
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Problembar, translated from ShylMShC/MskJ
A.Holeoule type: mRNA
A.Kosidues: 1-70 sSTA>
A.Cross-reterences: EMBLUB3192: NID:q+d18652: PID:q+d18654
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RrStathakis, P.S.: Hoover, K.H.: You, Z.: Bryg
submitted to the EMBL Data Library, July 1998
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C:Species: Homo sapiens (man)
C:Date: [6 Ju] 1999 #Sequence_revision 16 Jul 1999 #text_chande 21 Jun
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Best Local Similarity
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523 ASHEDAAAATKNAGQAVIIVAQYKPEEYSKEEAKIHIILKEDMMNSSISSGSGSLKISOKK 582
                                                                                                                                                                                          166 EHHEKAVELLKAAKOSVKLVVRYTPKVLEEMEAREEKLR------TARRROOO 212
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Local Similarity 41.4%; Pred. No. 4.8e-07;
thes 41, Conservative 19, Mismatches 38; Indels 1
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Approximately discrete medical 1950; MID:a41245; PIDM:AAA79976.1; PID:a41215; ECONOPERIAMITY: discretare termor suppressor: didF domain hamology, guanylate F.229 307/19901; POR domain howelt by 2007; ECONOPERIAMITY CORP domain howelt by 2007; ECONOPERIAMITY CORP domain howelt by 2007; ECONOPERIAMITY CORP. ECONOPERIAMITY CORP. ECONOPERIAMITY CORP.
                                                                                                                                                                                             C:Keywords: alternative splicing; duplication F:229-207,9weain: C:CF domain bed-eg: 0.021
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Cospecies: Ractual nor entres provision 16 Jul 1996 #text_change 11 Jun 2000
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J. Neurosei. 15, 2354-2366, 1995
                                                                                                                                                          F: 324 - 402,700main: GLGF domain homology .GLG2
                                                                                                                                                                                                                                                                                                                       A;Cross-references- CDB-303078; OMIM-601014
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            Smore 192:
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            Length 926
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A:Molecule type: mRNA
A:Residues: 1-2054 +ULL>
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      A.Gross n. Fereness. EMBL.AJ001200, MID.42909978, PIDMLOAA04681.1, PID.42959978
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                                                                                                                                A. Accession. T46612
                                                                                                                                                      A. Reference number: 223104; MUID: 98196865
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PEBS Lett. 424, 63-68, 1998
A/Title: Clothy and characterization of MUFF), a novel
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidaes. 1 2005 .81M
A;Cross reterences. EMBL.AJ131869. NID.44158877, iIDX:CAA18523.1. FID.44158878
A;Experimental source: Strain CS7/BL6 X CBA FI; whole brain
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ArAccession: T30259
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P.Singland, E.R., 2015ab, P. Cenomics 59, ICC 104, 1399
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C.Species. Mus musculus (house mouse)
                                                                                                                                                                  multi PDZ domain protein 1 - rat
C;Species: Rattus norvegicus (Norway rat)
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                                                                                                                                  C:Date: 18 Feb 2000 #sequence_revision 18 Feb 2000 #text_change 21 Jul 2000
                                                                                                                                                                                                                                                                            RESULT 13
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submitted to the EMBL Data Library, January 1996
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A:Reference: FMBL_26875; PICKL/MAGL/ECT.L. 3/1688.3838.322.
A:Reference: FMBL_26875; PICKL/MAGL/ECT.L. 3/1688.3838.322.
C:Species: Caenorhabditis elegans
C:Date: 20-Sep 1999 #Sequence_revision 20-Sep 1999 #text_change 20 Sep-1999
C:Accession: T16191
R:Bentley, D.
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C/Species: Caenorhabditis elegans
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ArStatus: preliminary, translated from ShyTHBEZTDHO
ArMolecule type: DNA
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A;Description: The sequence of C. elegans cosmid F27D9.
A;Reference number: Z18473
A;Accession: T16191
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Job time: Search completed: May 7, 2002, 12:42:04

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OM protein - protein search, using sw model

Run on: May 7, 2009, 12:41:46; Search time 10.8 Seconds (without allgamments) 791.010 Million cell updates/sec

Title: Perfect score: Sequence: US-09-909-005-1 1170 1 MLKPSVTSAPTADMATLTVV

LLIQQQQQQQQQQQTQQNHMS 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

100059

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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EMBL; U49049; AAB53243.1; EMBL; U59717; AAC55643.1; EMBL; U59717; AAC55643.1; EMBL; U59718; AAB48562.1; EMSL; 012959; 1PDK. InterPro; IPECCO619; Guanglate_kin. InterPro; IPECCO619; Guanglate_kin. InterPro; IPECCO478; PDZ.	this SWISS-beb entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL cutstation. The European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in an way modified and this statement is not removed. Usage by and for commodicial collings pulses a license its energy (An letty [Ann isback by Long and to commodicial collings pulses a license its energy (An letty [Ann isback by Long and Lo	SEQUENCE FROM N.A.  ITTO M. Hata Y., Takai Y.;  SUBMITTAL (SHE 1995) L. LIA LMEL, ZALDINA, FOBJ databases.  SUBMITTAL INTERACTS WITH THE CYTCPLASMIC TAIL OF RHEA RECEITOR  SUBMITS AS WELL AS POTASSIUM CHANNELS.  SIMILARITY CONTAINS 3 FOAZTOR LOMAINS.  SIMILARITY CONTAINS 3 SHOULDHAINS.  SIMILARITY CONTAINS A SUANYLATE KINASE-LIKE DOMAIN.  SIMILARITY BELLONGS TO THE MAGGK FAMILY OF CELL JUNCTION PROTEINS.	SEQUENCE PROM N.A.  MIDCHIN GC19375, Premed ACC113;  Rechman A.E., Chao D.S., Gee S.B., McGee A.W., Graven S.E.,  Rechman A.E., Chao D.S.,  Subtiliano D.R., Wu Z., Huang F., Xia H., Peters M.F.,  Froehner S.C., Bredt D.S.;  "Interaction of intric oxide synthese with the postsynapth density  protein PSD 95 and alphal syntrophic mediated by PDE domains.";  Cell 84.757 767(1996).	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE 96310881; PubMcd-8755482; Kim E . Cho K.o., Pothschild A., Shong M.; "Heteromultimerization and NMDA receptor-clustering activity of Chapsyn [10, a member of the PSD 95 family of proteins."; Neuron 17:103-113(1996).	,

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RESULT 2
DLG2_HUMAN
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Matches 51
                                                                                       DLG2_HUMAN STANDARD; PRT: 870 AA (015700; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 20-AUG-2001 (Pol. 40, last appointing update)
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                  Homo sapiens (Human).
Eukaryota; Metacoa, Cherdata, Cianiata, Vertebrata, Eatele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NEBI_TaxID~9606;
                                                                       HOMOLOG 2).
                                                                             20-AUG-2001 (Pol 40, last annotation update) CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (DISCS, LARGE
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PROSITE: PS5052; GUANYLATE_FINASE_2: 1.
PROSITE: PS50002; SH3; 1.
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SMART; SM00228; FD2; 3;
SMART; SM00326; SH3; 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00625; Guanylate_kin; Pfam; PF00595; PDZ; 3. Ptam; PF00018; SH3; 1.
SEQUENCE FROM N.A
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                                                                                                                                                                                                                            460 FLORGDOLLSVNGTDLEGASHEQAAAALKGAGQTVTIIAQYQEEDYARFEAKIHDLEBOM 519
                                                                                                                                                                                                                                                                      401 ATROPSVTLQRAISLEGEPPKVVIHKGSTGLGFNIVGG-EDGEGTFVSFILAGGPADI SC
                                                                                                                                                                                                                                                                                          88 ATAKATVAAFAASEGHSHPRVVELPKTDEGLGENVMCCKFONSPIYISETTPGGVAERHG 147
                                                                                                                                                                                                         ----- TARRRQQQQLLIQ 217
                                                                                                                                                                                                                                                GLKEGDOLLSVNCVSVEGEHHEKAVELI MAAKESVKLVVEYTEYVLESMEABEEKLE
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51; Conser
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                                      Chardata, Chamiata, Vertebrata, Euteleostomi,
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35.7%; Pred. No. 1.5e 08;
34; Mismatches 54,
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R > P (IN SEF 2).

A -> D (IN REF 2).

A -> D (IN REF 2).

A -> S (IN REF 2).

A -> S (IN REF 2).

H -> N (IN REF 2).

L -> Q (IN REF 2).

K -> A (IN SEF 2).

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KR -- NG (IN REF 2).
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PDZ 2.
PDZ 2.
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CUANYLATE KINASE.
CUANYLATE KINASE.
VR -> IL (1N REF. 2).
1 > M (IN REF. 2).
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Best Local
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P31007;
01-JUL-1993 |
01-JUL-1993 |
30-MAY-2000
                                                                DIGI_DRUME
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DOMAIN
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PROSITE: PS50052; GUANVIATE_KINASE_2; 1.
PROSITE: FS50105; EUZ, 3.
PROSITE: PS50002; SH3; 1.
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SMART; SM00028; FDD; 3.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00625; Guanylate_kin; 1. Ffam, FF30595; PDZ; 3. Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96310881; PubMed=8755482;
Kim E., Cho K.-O., Rothschild A., Sheng M.;
"Heteromultimerization and NMPA receptor-clustering activity of
Chapsys:110, a member of the PSD-95 family of proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3 domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIRSP, Q12959; 1PDR.
MIM; 603583; -.
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-1: SIMILARIIY: CONTAINS I SH3 DOMAIN.
-1: SIMILARIIY: CONTAINS A GUANYLAIE KINASE-LIKE DOMAIN.
-1: SIMILARIIY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
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I FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMUA RECEPTOR
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interPro; iPR001452;
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                                                                                                                                                                                  210 0000LLIQ 217
                                                                                                                                                                                                                 475 LEGASHEQAAAALKGAGQTVTITAQYQPEDYAPFEAKIHDLPEQMMNHSMSSGSGSLETN 534
                                                                                                                                                                                                                                                                                                                                                                                                                                  [Eccal
                                                                                                                                                                                                                                                163 VEGEHHEKAVELLKAAKDSVKLVVPYTPKVLEEMEARFEKLE---
                                                                                                                                                                                                                                                                                                                   163 HSHFEVVELFKTDEGLGFNVMGGKEÇNSPTT1SFTTFBGGVAEFHGGLKFGLG/LLFVWLVS 162
                                                                                                                                                                                                                                                                                                                                                  385 GLLPDSEMTS----HSQHSTATRQPSMTLQRAVSLEG---
                                                                                                                                                                                                                                                                                                                                                                                  43 GEVPVHKLQSLKKVLQSEFCTAIREVYQYMHFTITVNGCPEFFARATAKATVAAFAASEG 162
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(Rel. 26, Created)
(Rel. 26, Last sequence update)
(Rel. 39, Last annotation update)
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                                                                  STANDARD;
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29.3%;
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SMART: SM00228; PDE; 3.
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                                                                                                                                                                                                                                                                                                                  Transducer; SH3 domain; Alternative splicing; Repeat
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InterPro, 1PR000619; Guanylate_kin.
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11- FUNCTION: LOSS OF THIS PROTEIN CAUSES LARGE MAGINAL DISKS BY ALLOWING NEODELASTIC OVERGROWTH. THE PERSENCE OF A GUANYLATE KINASE DOMAIN SUGGESTS INVOLVEMENT IN ADEQUATE CELLULAR ADHESION AS WELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Woods D.F., Bryant P.J.; "The discs large tumor suppressor gene of Drosophila encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ephydroidea: Drosophilidae: Drosophila
NCBI_TaxID-7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00545; PDZ;
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SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS A GUANYLATE KINASE-LIKE DOMAIN.
SIMILARITY: HELONGS TO THE MATHE FAMILY OF CELL JUNCTICH PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AHUNDANTLY EXPRESSED.
TISSUE SPECIFICITY: BROAD SPECIFICITY. ABUNDANTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AS SIGNAL TRANSPIRATION TO CONTROL CELLULAR PROLIFERATION, THE PROTEIN PLAYS A CRITICAL POLE AT SEPIATE JUNCTIONS IN CELLULAR GROWTH CONTROL DEFING LARVAL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: LEADS TO DIFFERENT FORMS OF THE ENOTEIN, THAT IS MOST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: CYTOSKELEION-ASSOCIATED, LOCATED AT THE CYTOPLASMIC FACE OF THE MEMBRANF IN THE CYLLULAR BLASTODERM AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPITHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BECOMES ASSOCIATED WITH SEPTATE JUNCTIONS WHICH BEGIN TO FORM BETWEEN EPITHELIAL CELLS AT THE TIME OF DORSAL CLOSURE. IN ADI
      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00625; Guanylate_kin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              012989; Ibbh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATED AT THE APTCAL-LATERAL MEMBRANE BOUNDARY OF
         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                   154
486
                                                                                                                                                                                768
                                                                                                                                                                                                                                126
244
566
                                                                                                                                                 102468 MW;
                           17.8%; Score 208.5; DB 39.3%; Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3
         2
                                                                                                                                                                                                                                                           PDZ 1.
PDZ 2.
                                                                                                                                                                         GUANYLATE KINASE
                                                                                                                                                                                                                                   PDZ 3.
      Mismatches
                                                                                                                                           BF87A4262F1B6AD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no restrictions on one as its content is in no
                                                         DB 1; Length 960,
      49;
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   indels
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Gaps
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RESULT 4
DLG3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.ish-sib-ch/data-anaco.or send an email to licensewish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Buman).
Eukaryota, Matalba, Chordata; Craniata; Vo
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                             MIM; 300189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncogene 14:2425-2433(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila discs large (dly) tumor suppressor protein interacts with the APC protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE 97302623; PubMed-9188857;
Makhoo K., Kuwahara H., Masuko H., Nishiyama Y., Morisaki T.
Sasaki J., Nakao M., Kuwano A., Nakata M., Ushio Y., Saya H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLG3 OF KIAA1232.
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01-NOV-1997 (Rel. 35, Last sequence update)
20-ANO-2001 (Rel. 40, Last annotation update)
PRESYNAPTIC PROTEIN SAPIO2 (SYNAPSE-ASSOCIATE) PROTEIN 102)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q92796; Q9ULT8;
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                                                                                                                                                                                                                                                                                             interPro; iPR000619; Guanylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Prediction of the coding sequences of unidentified human genes
The complete sequences of 100 new cDMA clones from brain which o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20039619; PubMed=10574462;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NEURCENEGOCKINE-DIG) (NE DLG) (DISCS, LARGE HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMIA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 330-817 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and characterization of NE-dlg: a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        525 ELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVILLAQYRPEEYNKFEAKIQELK 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 ATAKAIVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISKIIPGGVAERIG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILAPITY: CONTAINS A GUARYLATE KINASE-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE MAGUE FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT NR2B (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                large proteins in vitro."; Res. 6:337-345(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONTRACTOR TO A STANDARD TO A STANDARD SERVICE AND A STANDARD SERVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVPPGTPRAVSTEDITTRAPRTITIQKOPQGIGENIVGG-FDGQGIYVSFILAGCPADLDS 5.24
                                                                                                                                                                                                                                                                                                                                                                                                                                U49089; AAB61453.1;
                                                                                                                                                                                                                                                                                                                                                                Q12959; 1PDR.
                                                                                                                                                                                                                                                                                                                                                                                                    AB033058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T., Ishikawa K.-I., Kikuno R., Hirosawa M., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                BAA86546.1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions on one as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage by
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Fidam: PF00625; Ghanylate\_kin; 1. Ptam; PF00595; PDZ; 3. Pfam; PF00018; SH3; 1. SMAPT; SM00072; GuKc; 1.

InterPro; IPR001452;

SHU

InterPro; IPRO01478; PDZ

SMART; SM00228; PDZ; 3. SMART; SM00326; SH3; 1.

PROSITE; PS00856; GUANYLATE\_KINASE\_1;

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Best Local :
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
          MGD; MGI:1888986; Digh3.
InterPro; IPRO90619; Gwarylute_kin.
InterPro; IPRO91478; PDZ.
InterPro; IPRO91474; PDZ.
InterPro; IPRO91474; PDZ.
Pfam; PP09625; Guarylate_kin; 1.
Pfam; PP09595; PDZ: 3.
                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6; TISSUE-Brain; Kohmura N. Makino S., Yagi T.; Kohmura N. Makino S., Yagi T.; Submitted (AUG-1996) to the EMBL/French FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMNA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PRESYNAPTIC PROTEIN SAPIÚZ (SYNAPSE-ASSOCIATED PROTEIN 102) (DISOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                            SUBUNIT NEZE.

11 SIMILARITY: CONTAINS 3 PDE/ZHE DOMAIN:

11 SIMILARITY: CONTAINS 1 SH3 DOMAIN.

12 SIMILARITY: CONTAINS A CHARVIATE KINASP-LIKE DOMAIN.

13 SIMILARITY: BELON'S TO THE MAGRIK FAMILY OF CELL HUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLG3_MOUSE
P70175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3 domain; Repeat.
                                                                                                                                                                       use by son profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryeta, Metarea, Cherdata, Charlita, Vertebrata,
Mammalia, Butheria, Rodentia, Sciurognathi, Maridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DECRITE,
                                                                                                               EMPL: E87117; PAA13249.1;
                                                                                                                                              or send an email to licensewish-sib.ch).
                                                                                                                                                           entities requires a license agreement (see http://www.isb-sib -h/annonnes
                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                  This SWISS-PECT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLG3 OR DLGH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LARGE HOMOLOG 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 PROVETERKEDEGLIGENOMGGKEQNSPTYTISHTTPGGOAFRHGGLIKBGDQTLISONGOSOFG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               443 ATHEQAAAALKRAGQSVTIVAQYRPEEYSRFESKIHDLR 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 PRKIILHKGSTGLGENIVGG-EDGEGIEVSFILAGGPADLSGFLREGDRILSVNGVNLFN 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
PF00018;
                                                                                                      012959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; PS50052; GUANYLA
; PS50106; PD2; 3;
; PS50002; SH3; 1;
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628
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226
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                                                                                                      1PDR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Mismatches
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DEFGLSDDYYGAKNI -> SIKEKKKKSFRLSRKERFYKSK
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PRHMLAEEDFT -> AARPERGAMERARKFSGSGLAMGLGS
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GUANYLATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENMAQESSIQEQGVTSNTSDSESSS (IN KEF. 2).
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SMART, SM00326, SH3; 1.
PROSITE; PS00856; GUANYLATE_KINASE_1;
PROSITE; PS50052; GUANYLATE_KINASE_2;
PROSITE; PS50056; PDZ; 3.
PROSITE: PS50106; PDZ; 3.
                                                                               the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as list scatter, is in some modified and this statement is not removed. Usage by and for commerciations in equipment of the profit size of the biometers of the statement of the biometers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "SAP102, a novel postsynaptic protein that interacts with NMDA receptor complexes in vivo.";
Neuron 17:255-265(1996).
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PRESYNAPTIC PROTEIN SAPI02 (SYNAPSE-ASSOCIATED PROTEIN 102) (PSD-95/SAPSO PELATED PROTEIN 1) (UISOS, LARGE HOMOLOG 3).
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DOMAIN 149
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                                                                                                                                                                                                 This SWISS-FPOT entry is copyright. It is produced through a collaboration between the Swiss Institute of Hioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Irie M., Hata Y., Takai Y.;
Schmitted (Shr-1900) to the EMSL, Wiener & JUBEL detabases
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Eukaryeta, Metarea, Cher
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                                                       or send an email to license@isb-sib.ch).
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-!- SIMILARITY: CUNIAINS A GUANYLAIE KINASE-LIKE LOMAIN.
-!- SIMILARITY: BELONGS TO THE MASUK FAMILY OF CELL JUNCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garner C.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mueller R M , Kistner H , Kindler S., Chung W J , Kuhlendahl S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96374358; PubMed=8780649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA RECEPTOR
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(See hitp://www.ich.sib
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EMBL; U50147; AAA93031.1;

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                             this SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial cutities requires a license agreement (See Fig. 128) in the total continuous continuous
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kohmuta N., Yaqi I.;
Submitted (MAY-1995) to the EMBL Centrel (Tore 11 Bees)

11 FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMIA RECEPTOR SUBMITIS. MAY HE INVOLVED IN SYNAPLOGENESSIS (BY SIMILARCITY).

11 SUBCELLULAR LOCATION: CONCENTRATED AT SYNAPTIC JUNCTIONS PRIMARILY ON THE EPERYMAPTIC SIDE (BY SIMILARCITY).
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    or send an email to licensee spesib ch)
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Enkaryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi;
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20-AU0-2001 (Rel. 40, Last annotation update)
PRESYMAPTIC DENSITY PROTEIN 95 (PSE-95) (PRESYMAPTIC PROTEIN SAP90)
(SYNAPSE-ASSOCIATED PROTEIN 90) (DISCS, LARGE HOMOLOG 4).
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SMART; SM00228; FDZ; 3.
SMART; SM00326; SH3; 1.
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InterPro; 1PR001478; PDZ.
InterPro; 1PR001452; SB3.
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STRAIN-DBA/2: TISSUE-Brain;
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SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
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43.4%; Pred. No. 2e
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MISSING (IN SHORT ISOFORM).
340A9046C7BB96DB CR064;
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Best Local Similarity
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SEQUENCE
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01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
20-AUC-2001 (Rel. 40, Last annotation update)
FRESYMAFTIC DIRSITY FROIDIN 95 (FSD 95) (FRESYMAFTIC FROIDIN SALSO)
(SYNAPSE-ASSOCIATED PROIDIN 90) (DISCS, LARGE HOMOLOG 4).
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NIVWOG
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SMART: SM00028: PDZ; 3.
SMART: SM00028: PDZ; 3.
SMART: SM0028: SH3; 1.
SMART: SM00326: SH3; 1.
SMORT: SM00326: SH3; 1.
SMORT: SM00326: SH3; 1.
SMORT: SM00326: SMORTIAIE_KINASE_1:
PROSTIE: PS50056: FDZ; 3.
STRAIN-WISTAR KYOTO, TISSUE A
                                                                                                                                        Kistner U., Wenzel B.M., Veh K.W., Cases-tanghoff C., Garmer A.M., Appeltaner U., Voss B., Gundelfinger E.D., Garmer C.C.; "SAP99, a rat presynaptic protein related to the product of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; Q12959; IPDR.
MGD; MG1:1277959; Dlqh4.
                                                                                 Drosophila tumor suppressor gene dlg-A.";
J. Biol. Chem. 268:4580-4583(1993).
                                                                                                                                                                                                                                                                                                                                                                         "The rat brain postsymaptic density fraction contains a homolog of
the Drosophila discs-large tumor suppressor protein.";
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                                                                                                                                                                                                                             MEDLINE-93186749; PubMed 7680343;
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InterPro: IPRO01478; PDZ.
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                                                                                                                                                                                                                                                        STRAIN SPRAGUE-DAWLEY: IISSUE Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN SPRAGUE-DAWLEY: FISSUE Brain;
INE 9294#233: PubMed 1419001;
                                                                                                                                                                                                                                                                                                                                                                                                                                     TO., Hunt C.A., Kennedy M.B.;
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Pred. No. 5.3e-07;
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Pfam: PP00525; Chamylate_Klb: 1.
Pfam: PP005455; DDZ: 4.
Pfam: PP00418; SH3: 1.
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SMART; SM00228; PDZ; 3.
SMARI; SM00326; SH3; 1.
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-1- SUBGRITHER FORATION: CONCENTRATED AT SYNAPTIC FUNCTIONS DEIMARILY
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311 PRRIVIHROSTOJ GENIVOG-PDOFGIFISETI AGOPANESGELPKODOJI SVNGVDERN 369
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SIMILARITY: CONTAINS I SH3 DOMEN.
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SIMILARITY: BELOWGS TO THE MAGUK FAMILY OF CHIL JUNCTION PROTEINS.
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                                                                                                                                Similarity
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                                                                                                       19: Mismatches
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M => L (IN KEF 2).
S => T (IN KEF 2).
GVGNGH - ALDTSI (IN KEF 2).
A -> C (IN KEF 2).
S -> T (IN KEF 2).
LICOPKURANUOLLSEF -> ISLDEP
                                                                                                                             Score 196.5; DB 1: Length 724; Pred. No. 5.3c 07;
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GKH -> RDQ
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DLG4_HUMAN
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01:NOV-1997 (Red. 35, Greated)
30:MAY 2000 (Red. 39, Last sequence update)
20:AUG-2001 (Red. 40, Last annotation update)
FRESTMARTIC DURSITY PROTEIN 95 (PSD-95) (DISCS, TARGE HUMBIAG 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss institute of Bioinformatics and the EMBs outstation the European Bioinformatics Histitute. There are no restrictions on it may be now postly institutions as long as its content is in no warmoulified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce.
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                                                                                                                                                                                                                                       HISSP: 012959
MIM; 602887;
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Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMIA RECEPTOR SUBDINITS. MAY HE INVOLVED IN SYNAPTOGENESIS.
-1- SUBCIDLULAR LACATION: CONCENTRATED AT SYNAPTIC JUNCTIONS PRIMARILY ON THE PRESYNAPTIC SIDE (WAS GRIGINALLY THOUGHT TO BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Breaman J.E., Bredt D.S., Parkinson J.E., Manzana W.E., Memlary J.A.;
Subwitted (AUG 1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PISSUE Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genomic organization of human DLG4, the gene encoding postsynaptic density 95.";
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Pfum: PP00625; Guanylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: UB3192: AAC52113.1; =:
EMBL: AF156495: AAD56173.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to licensegisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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S.Lmitted (UUL 1998) to the EMBH, TedBank, 94 F.L. databases
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                                                              InterPro: IPR001452; SH3
                                                                                                                      laterPro, iPsotd478,
                                                                                                                                                                                     InterPro: IPR000619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS FROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                     Q12959; 1PDR.
                                                                                                                                                                                                                                                                                                                                                                   U68138: AAB07736.1;
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Ptam; PF00595; PDZ;

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CONFITTOT
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Martatia S.M., Chishti A.H., Liddingt
"Crystal structure of a PDZ domain.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lue k.A., Marfatia S.M., Branton D., Chishti A.H.: "Cloning and characterization of hdfg: the buman homologue of topocophila discs large tumor suppressor binds to protein 4.1."; Proc. Natl. Acad. Sci. U.S.A. 91.9818 9822(1994).
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini: Homiotaae: Homo
                                                                                                                                                                                                                                                                                                                         Nature 382:649-652(1996)
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SMART: SM00229; PP?: /
SMART: SM00326; SH3; 1
                       This SWISS-PMOT entry is copyright. It is preduced through a collaboration between the SWiss institute of Bioinformatics and the EMSL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE 96338231; PubMed-8757139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE 95024052; PubMed 7937897;
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  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-KAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 460-555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 PHEFAVELLEAARISVELVAPTEFALISHMEVELTS 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 PRKIVIHROSTOLOPNIVOH-FPGROJFISETLAGGEADLSGELKEGE, LLSVNGVELLEN 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 ASHEQAATALKNAGGTVTTTAQYKPEEYSKFEAKTHDLK 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.01 DRAKAPURASTIT POLGSFPTOCHERVACCET TEST ** SW***SWARK POLG FING HAAAREL BULL
                                                                                SUBUNITS. ASSOCIATES WITH PROTEIN 4.1.
ALTERNATIVE PRODUCTS: 2 ISOFYMMS; 1 (SHOWN HERE) AND 2, ARE
PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: CONTAINS 3 PDZ/DHR 19 MAINS.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: BELIGHES 1 SH3 MACHE FAMILY OF CHEL JUNETERS.
SIMILARITY: BELIGHES 10 THE MACHE FAMILY OF CHEL JUNETERS.
                                                                                                                                                                                                                                                                                               FUNCTION: INTERACTS WITH THE CYPOPLASMIC TAIL OF NMDA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50106; PDZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399
767 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85429 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       Surclitte M
                                                                                                                                                                                                                                                                                                                                                                                Liddington R.C.;
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VIV -> EFR (IN KEF, 4).

GEQ > AG1 (IN KEE, 4).

; BC1919159E65B2D9 CRC64;
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PDZ 2.
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  There are no
                                                                                                                                                                                                                                                                                                                                                                                                       Para s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 767;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE Brain: MEDILINE 95:98112: Papered 78:91172: MacDiline 95:98112: Papered 78:91172: MacDiline 18.5. Kisther 0.7. Veb E.W., Cases-Landhoff 0., Beeker Br., Gundelliner E.D., Garner C.C.; "Molecular characterication and spatial distribution of 8AP97, a povel presynaptic protein homologous to 8AP90 and the brosophila dises-large Lumor suppressor protein.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N I VWOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSTIE: PS00856: GUANYLATE_KINASE I: PROSTIE: PS50052: GUANYLATE_KINASE_J: PROSTIE: PS50106: PDZ: 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as lond as its content is modified and this statement is not removed. Usage by and for entire transfer as the statement (***) its asset to be statement (***) its asset to be statement (***).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SH3 domain, Repeat, Alternative spliting, DOMAIN 224 310 FDZ 1. 5CMAIN 319 405 FLZ 2.
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SMART; SM00228, FDZ; 3.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, FF00625, Guanylate_kin; Pfam, PF00595; PDZ; 3. Pfam, PF0001B; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U13897; AAA50599.1;
EMBL; U13896; AAA50598.1;
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                                                                                                                                                                                                                                                                                                                                       Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; kodentia; Sciuroquathi; Muridae; Murinae; kattus
                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norverlicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LARGE HOMOLOG 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS50002; SH3; 1
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                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         NCBI_TaxID 10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             583 SLYVK 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              523 ASHROAAAALKNAGQAVIIVAQYRPEEYSRFEAKIHDLKEOMMNSSISSGSGSLRISGAR (542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIGURE AND LEAAKING VET VVET PROTEKTIEEMBAPBEKLIP - - - - - - - - TARPROOF 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Conservative 23; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             904 AA; 100354 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 192; DB 1; Lenath 904
Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EITTIMUSE DE . "VIM EFFERGRÄFERRICKERIGS
EUETSDAMO (IN ISOFORM 2).
W) H78798B6BB0920D4 (NC64)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDZ 3.
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                                                                                        RESULT 12
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N I VWOOL
012923; Q15263; Q16826; Q15264; Q15265; Q15159;
20-AUG-2001 (Ref. 40, Created)
20-AUG-2001 (Ref. 40, Last sequence update)
                                                     PIND_RUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART: SM00072; GuKC; 1.
SMART: SM00228; PDZ; 3
SMART: SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3 domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50106; PDZ; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE: PS00856; GUANYLATE_KINASE_1; 1. PROSITE: PS00852; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF000595; PDZ; 3. Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00625; Guanylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP: Q12959; AAA79976.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license areadent (S or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on use by morpholit institutions as but as its content is in ac-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: 1PR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR000619; Guanylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
                                                                                                                                          582 SLYVR 586
                                                                                                                                                                                                        522 ASHEQAAAALKMAQAVTTVAQAVTERTYSFELAKIIBALFEIDMNESVSSOSOSLICTSQKE 581
                                                                                                                                                                                                                                                                        463 PRKVVLHROSTOLOFNIVEG-FLOEGIFISFILAGGPADLSOFIPKODPITSVNSVDIPA 521
                                                                                                                                                                        213 QLLIQ 217
                                                                                                                                                                                                                                          166 BHBEKAVELLKAAKDSVKLVVETTEKVLEEMEARFEKLE------
                                                                                                                                                                                                                                                                                                       106 PRVVELPKTDEGLGFNVMGGKEDNSPIYISPITPGGVAERHOGLKEGDOLLSVNGVSVEG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurosci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS I SHE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: IN CHITURED T84 CELLS, IT IS RESTRICTED TO THE CYTOPLASMIC SUFFACE OF THE PLASMA MEMBRANES BETWEEN ADJACENT CELLS. BUT NOT AT THE EDGES OF CELLS LACK RING CELL-CELL CONTACT. TISSUE SPECIFICITY: PRESENDED TO NERVE TERMINI OF EXCITATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: INTERACTS WITH THE CYTOPLASHIC DELL OF MINA RECEIVE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: RELONGS TO THE MAGHE FAMILY OF CELL TINCTION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS A GUANYLATE KINASE-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYNAPSES. IN OTHER BRAIN RESIGNS, SAP97 IS FEBRUTH AND ALORG BUNDLES OF UNMYELINATED AXONS. SAP97 IS NOT RESTRICTED TO THE CNS BUT IS ALSO PRESENT AT THE BASAL LATERAL MEMBRANE BETWEEN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL ADHESTON.
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                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                     CTANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            404
545
650
911
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                                                                                                                                                                                                                                                                                                                                                        16.4%;
35.2%;
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                                                                                                                                                                                                                                                                                                                                                                          Score 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY - ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUANYLATE KINASE.
                                                     1781,
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ... N :--
                                                     2485 AA
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                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                       TARRECCO DID
                                                                                                                                                                                                                                                                                                                                        14; Caps
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PIOCHEMISTRY 39:2572-2580(2000).
-!- FUNCTION: BINDS TO A REGATIVE RESULATORY DOMAIN IN FAS THAT INHIBITS FAS-INDUCED APOPTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maekawa K., Imagawa N., Nagamatsu M., Barada S.;
"Melecular eleming of a novel protein tyrosine phosphatase containing
a membrane-binding domain and GLGP repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A nevel protein-tyrosine phosphatase with homology to both the cytoskeletal proteins of the band 4.1 family and junction-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2001 (Ref. 40), Last annotation update)
F8-IEIE lin Alta idősinAlALE, Rok Köllfrok fron lin (b) 3.1.3.44)
(F8-IEIE lin Alta idősinAlALE, Rok Köllfrok fron lin (b) 4.1.3.44)
(PROFEIN INACINE DEĞSINALASE E) (F1F-EL) (F1F-BAS) (PROFEIN TYROSINE PHOSPHATASE E)
PHOSPHATASE PIPLI) (FAS-ASSOCIATED PROTEIN-TYROSINE PHOSPHATASE E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saras J., Claesson-Welsh L., Heldin C.-H., Gonez L.J.; "Cloring and characterization of PTPL1, a protein tyrosine phosphatase with similarities to cytoskeletal-associated proteins."; J. Biol. Chem. 269:24082-24089(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Fibroblast;
MEDLINE 95014139; PubMed=7929060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE Loukomia; PobMod-8287977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE 94350988; PubMed-8071359; Banville D., Ahmad S., Storco R., Shen S.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eskaryola: Metassa; Chordata; Crasiata, Vertesiata; E
Mammalia, Eutheria, Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and its interactions with C-terminal peptides from the Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Exploy 1. Schring K., Ekiel 1.;
"Solution structure of the PMZ2 domain from human phosphatase hPTP1E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE 20170882; PubMed-10704206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang H.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pancreas;
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                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID 9606;
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SIMILARITY: BELOROS TO THE NON-RECEIVED ROLLARD OF THE FORTUNE
                                                                                                                                                                                                                                                                                                                    SUBCRILULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: PRESENT IN MOST TISSUES WITH THE EXCEPTION OF
                                                                                                                                                                                    TYROSINE PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                 PETAL BRAIN.
                                                                                                                                                                                                                                                                                  THE LIVER AND SKELETAL MUSCLE, MOST ABUNDART IN LUNG,
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modified and this statement is not removed. the European Biointormatics Institute.

non-profit institutions as long as its content

EMBL; U12128; AAB60339.1; EMBL; D21209; BAA04750.1;

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PROSITE: PS00661; BAND_41_2; FALSE_NEG.
PROSITE: PS50057; PAND_41_3; 1.
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PKINTS; PK00700; PKTYPHPHTASE.
PKINTS; PK00935; BAND41.
1369 VELIAKNUNSEGISVIGGVNISVRHGGIYVKAVIPQGAAESDGHIHKGDRVLAVNGVSEEG
                                  1309 ISBVIDYSDRODSBMDEATYSSSQUHQTVKQESSSSVNTSNKMNEKTESVSEPKEODTEE 1368
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                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative splicing;
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SMART; SM00228; PDZ; 5
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InterPro: IPk000242; IYr_prot_phphtae
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               109 VELPKTDEGLGFNVMGG----KEGNSPIYISKIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                      78 VNGCPEFRARATAKATVAAFAASEGHSHPR-------
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PSSO058: TYR_PHOSPHATASE_1: FIPSO058: TYR_PHOSPHATASE_FTP:
PSSO055: TYR_PHOSPHATASE_FTP:
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BAA04752.1; ·.
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SLUCY VARS (IN REF. 1).
MW: BUJERISE7066962B (B0544)
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                                                                                Fred. No.
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164 EGEHHEKAVELLKAAKUSVKLVVRY 188 : |: ||:||:| :| || ||:: 135 KNLLHQDAVDLEKNAGYAVSLRVOH 159 109 VELPKTERBLOLG, AVMOGNER

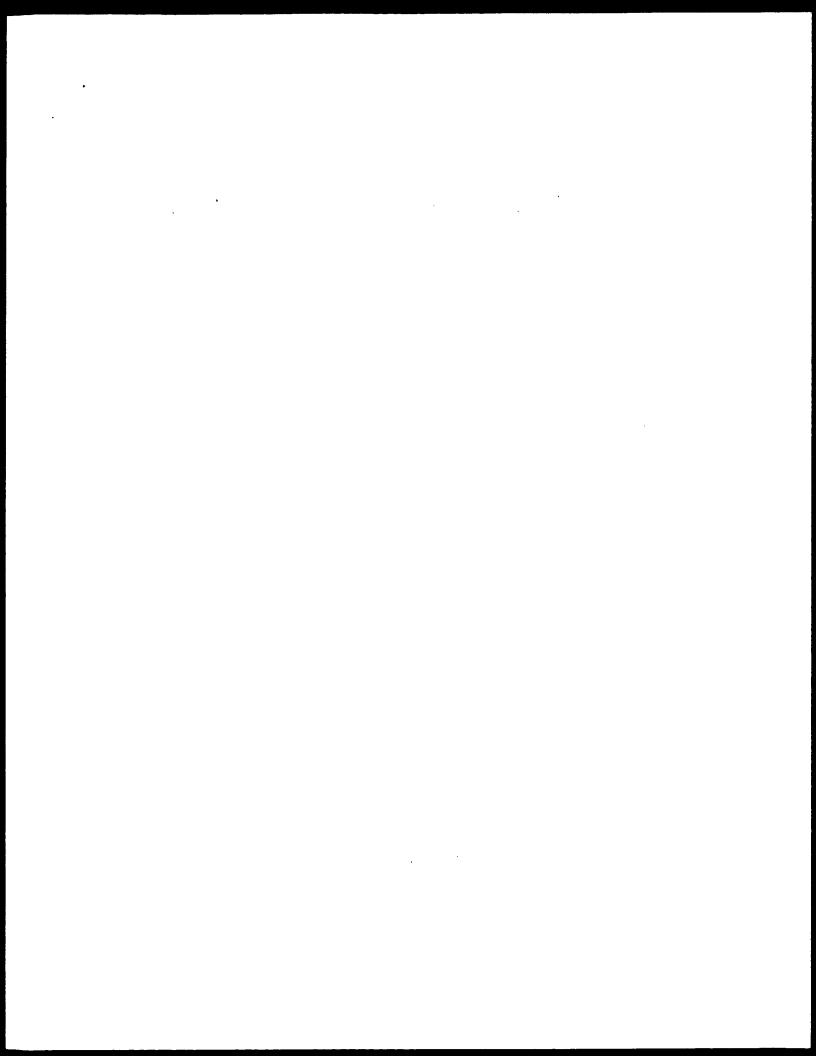
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Jin W., Wang Y., Yang H., Liao B., Ju G.;
"Production and characterization of monoclonal antibodies against numble: a novel PDZ protein.";
Submitted (AFF 1989) to the PDZ protein.";
SUBUNIT: HINDS SYNAPTOJANIN ZA.
-1- SUBCELLULAR LOCATION: MITOCHONDETAL OFFER REMOVED.
                                                                                                                                                                                                                                                         Mitochondrion; outer membrane; Irausmembrane
bemain 1 178 CYFORIASMIC (PO
TRANSMERM 179 159 FORENITAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Recruitment of an alternatively spliced form of synaptojanin 2 to
mitochondria by the interaction with the BM domain of a mitochond
outer membrane protein.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AUS-2001 (Rel. 40, Created)
20-AUS-2001 (Rel. 40, Last sequence update)
20-AUS-2001 (Rel. 40, Last annotation update)
20-AUS-2001 (Rel. 40, Last annotation update)
MIPSCHENDRIAL SCHER MEMBRAND FROMEIN 25 (NPW16).
                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR001478; PDZ: Pfam; PF00595; PDZ; 1. SMART: SM00J28; PDZ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bikaryota; Mctazoa; Chordata; Cianiata; Vertebrata; Euteleostom;
Mammalia; Eutlecia; Rodentia; Sciuroquathi; Muridae; Murimae; Rattus
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                                                                                                                                                                 SEQUENCE
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EMBL, AN260258; AAN70306.1; ALT_INII.
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                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE SPECIFIC TO SYNAPICJANIN 2A. SIMILARITY, CHITAINS I FUL/DHR DOMAIN.
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45; Conservative
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206 AA;
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161 P
22562 MW:
                            13.5%, Score 157.5; DB 1: 41.2%; Pred, No. 7.6e 05;
le: Mismatches 27:
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Bannert N., Avots A., Baier M., Serfling E., Kurth R.; "CA-binding protein factors, in concert with the coactivator GREB binding protein/Pack, control the indexion of the indexionation in T lymphocytos."; Proc. Natl. Acad. Sci. 9 S.A. 96:1541-1546(1999).
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30-NOV-1997 (Rel. 39, Last sequence update)
20 AUC 2001 (Rel. 49, Last annotation update)
INTERLEUKIN-16 PRECURSOR (IL-16) (LYMPHOCYTE CHEMOATTRACTANT FACTOR)
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                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR 1998) to the EMBL/GenPank/PORT databases:
-!- FUNCTION: SIMULATES A MIGRATORY RESPONSE IN CD4+ LYMPHOCYTES,
MONOCYTES, AND EQSINOFBILS. ALSO INDUCES T-LYMPHOCYTE EXPRESSION
OF INTERFERENT 2 PROEPTOP !!GAMD POR CM
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 502-631 FROM N.A.
Du Y., Du G.X., Hou L.H., Wang H.T.;
"cDNA sequence of interlepkin-16 cloned from human PRES.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Theodore A.C., Kornfeld H.: Theodore A.C., Kornfeld H.: "Molecular and functional analysis of a lymphoxyte chescattractant factor: association of biologic function with CD4 expression."; Proc. Natl. Acad. Sci. J.S.A. 91:5109-5113(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB-Peripheral blood;
TISSUB-Peripheral blood;
MEDIINE-94255486, Fubbod 7910967,
Cruikchack W.W., Seebel E.N., Nisat W., W. N., Nacke B.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enkaryota, Metacca, Chordata, Craciata, Vertebrata, Esteleostomi
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Home.
Pfam; PF00595, FDZ, 3. SMART, SMC0228, FDC, 2.
                                                                                                                                                                                                                   use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
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                                                     MIM: 603035;
                                                                                        EMBL; AF053412,
                                                                                                                                            EMBI; M90391; AAD04636.1; -
                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Interleukin-16 or not?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bannert N., Baier M., Werner A., Kurth R.;
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-1- SIMILARITOR: CONTAINS 2-FUZ/FHR FOMAINS
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CONFLICT
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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InterPro, FPR001478, PDE Pfam, PP005595, PDC, 1.
                                                                                  modified and this statement is not removed. Usage by and to obtain a requires a liberase agreement (Are byte j. www.ist sile
                                                                                                                                                                                                 SIMILARITY CONTAINS 1 PDZ/DHR DOMAIN
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Mammalia; Eulheria; Primates; Calarrhini; Hominidae; Homo.
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                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Placenta;
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2 Sequence 496 Application USZJO102800

3 GENERAL INFORMATION:
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                                                                                                                                                         SEQ ID NO 496
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TITLE OF INVENTION: Novel Human Kinase and Polynorleotides Encoding the Same
File REFERENCE: LEX-0323-PCT
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CURRENT FIXING FAIR 2002 M3-20
PRIOR APPLICATION NUMBER: US 60/277,168
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SUFTWARE: FastSEQ for Windows Version 4.0
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NUMBER OF SEQ ID NOS: 846
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SOFTWARE: Patentin Ver. 3.0
SECTION NO. 5965
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Best Local Similarity
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APPLICANT: JONES, Anissa L.
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E Similarity (4.3%; Pred. No. 0.000;
43; Conservative 17; Mismatches 42; Indels 7; Gaps
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DUFOUR, Gerard E.
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YAP, Pierre E.
                                                                                                                                                        YU, Jimmy Y.
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APPLICANT:

AMSHEY, Stefan R

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Best Local Similarity 28.2%;
Matches 29, Conservation 2
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UKASHKA, Michael E.
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LEWIS, Samantha
CHEN, Alice J.
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| RESULT | 2 | US 09 - 870 - 102 - 1 | Superior | 1, Application | UJ/09 870102 | Pattent NO. 6265547 | SUBURAL INFORMATION: | APPLICANT, Yee, Henry

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: GENERAL INFORMATION
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55.0%; Score 648.5; DB 3; Length 297,
Hest Local Similarity 70.6%; Pred. No. 1.1e-56;
Matches 127; Conservative 29; Mismatches 28; Indels 1; Caps
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APPLICANT: Au-Young, Janice
APPLICANT: Patterson, Chandra
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ORGANISM: Homo sapiens
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Patent No. 6265547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NOMBER: US/05/370,162
CURRENT FILING DATE: 1999-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Au-Young, Janice APPLICANT: Patterson, Chandra
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ZIP: 02ZIO
CHPUTEK KEZWABLE FORM:
MEDIUM TYPE: Floppy disk
CAMEGIEK. IBM PC compatible
CAMEGIEK. SYSTEM: PO-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: q1685067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: FRIMARY STRUCTURE AND FUNCTIONAL TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN TITLE OF INVENTION: TYROSINE PHOSPHAIASSES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CLAESSON-WELSH, LENA APPLICANT: HELDIN, CARL-HENRIK
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                                                                                                                                                                                                                                                                                       CAMPINATE :
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                                                                                                                            COMPUTER REALDBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HM PC COMPUTED:
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENTIETD & SACKS, E.G.
STREET: 600 ATLANTIC AVENUE
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                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TYROSINE PHOSPHATASES NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1154 VI 1155
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TELEPHONE: 617/720 3500
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FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFOFMATION
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OB/596,291
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THILE OF INVENTION: PRIMARY ST
INTLE OF INVENTION: EXPRESSION
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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US/09/100,804
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: Patent No. 6083721
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                                       NUMBER OF SEQ ID NoS: 49
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                APPLICANI: Saras, Jan
APPLICANI: Franzi, Petra
APPLICANI: Aspensirm, Pontus
APPLICANI: Heldinan, Dir
APPLICANI: Gomez, Lernel Jorqe
APPLICANI: Gomez, Lernel Jorqe
APPLICANI: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INLEFACIS WITH PIPLI
CHAE KEITENENCE: L0467/7030
CUKRENI AFPLICANI: NOMBEE, US/05/080,855A
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                                                                                                                                                                              EARLIER APPLICATION NUMBER: 08/805,583 EARLIER FILING DATE: 1997-02-25
                                                                                                                                                                                                                                                                                 CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2465 amino acids
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NAME: CATES, ENACHOR R.
RECISTRATION NUMBER: 31.616
FIFTERING; THE FYMERS: 1.48
TILLED MAGNICAL ON THICKMATION:
TELEPHONE: 617-720-2441
TELEFAX: 617-720-2441
LENGTH: 2466
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PCF-8894-09943-2
                                                                                                                                                                                                                                 PCT-US94-09943-2
    overy Match 15.4%; Score 180.5; DB 5; Bess Local Similarity 27.9%; Pred. No. 5.5e 09, Matches 51; Concervative 41; Mismatches 64,
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FELEX: 92-1742 EZEKTEL
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM, TC LOCTUS (FF
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                MollECULE TYPE: protein
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PRIOR APPLICATION DATA.
PRIOR 
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TITLE OF INVENTION:
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ALTORNEY/AGENI INFORMATION.
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                                                                                                                                                                                                                                                                                                                                                               TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 14.9%; Score 174.5; DB 4; Length 2037; Best Local Similarity 37.6%; Pred. No. 1.7e-08; Matches 38, Conservative 20, Mismatches 40, Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER FILLING DATE: 1998-05-08 NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/306, 998 CURRENT FILING DATE: 1999-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: MMSC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tavtiqian, Scan V. TETTLE GF INVENTION: MMSC2: An MMAC1 Interacting Protein
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HELDIN, CARL-HENKIK
THTLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
THILE OF INVENTION: PROBLESSION OF NUCLEOFIDE SECURICES FOR NAVEL PROTEIN
THILE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SECURICES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFFLIGARE GARAS, JAN
AFFLIGANE CLARSSON-WELSH, LENA
TOTTOANE CLARSSON-WELSH, LENA
CARL-HENKIK
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ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C
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                                             COUNTRY:
                                                                                                      STATE:
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COMPUTER READABLE FORM:

OPERATING SYSTEM: PO-DES/MS-DOS

MEDIUM TYPE:

Floppy disk

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                                                                                                                                                                                                                                                              APPLICANT: Croce, Carlo
APPLICANT: Canuani, Eli
TITLE OF INVENTION: Distriction and Irealment of Acute Leukemias
TITLE OF INVENTION: For Detection and Irealment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                     ADDRESS: Weederey, Washing, Entil Mackiewit.
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APPLICATION NUMBER
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                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 LLKAAKDSVKLVV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 GLOFNYMOGKEQ---NSPIYISRIIFGGVAEKHGGLKRGDQLLSVNGVSVEGEHHEKAVE 173
                                                                                                                                              STREET: one Liberty
CLIY: Philadelphia
              MEDIUM TYPE: Ploppy disk
COMPUTEK: IBM PC computible
OPERATING SYSTEM: POSTORS ONE-POS
                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 ILQNAPEDVILVI 77
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SOFTWARE:
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Patentin Release #1.0, Version #1.25
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**Sequence 54, Application PC/TUS9404496

**CEMERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (215) 568-419
TELEPAX: (215) 568-4449
INFORMATION FOR SEQ ID NO: (
                                                                   APPLICANT: Groce, Carlo
APPLICANT: Granani, Eli
APPLICANT: Canaani, Eli
IIILE OF INVENTION: Diadnostics, Therapeutics and Methods
IIILE OF INVENTION: for Detection and Treatment of Acute Leukenias
TITLE OF INVENTION: Resulting from Chromosome Abdormalities in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECOLL PARTY NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DeCKET NUMBER: THE TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION TOTAL
FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                CORRESPONDENCE ADDRESS:
                                                       NUMBER OF SEQUENCES:
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: sin
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ADDRESSEE: Norris
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              Words with Williams, Kinsty
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11-DEC-1991
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STATE

Pennsylvania

CITY: Philadelphia

W. (XXX):

One Liberty Place, 46th floor

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                                                                                                                                                                                                                                                                   SEQ ID NO 46
                                                                                   Best Local Similarity
Matches 40; Conserv
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 East Local Similarity 46.8%; Score 170.5; DB 5
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dean, Nicholas M. APPLICANT: Marcusson, Eric G. APPLICANT: Marcusson, Eric G. TITLE OF INVENTION: Antisouse Compound Modulation of Fas Mediated Signaling
                                                                                                                                                                                                                                                                                                     CURRENT FILING DAIE: 1999-04-12
NUMBER OF SEQ 1D NOS: 85
                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ISPH-0351
CURRENT AFFLICATION NUMBER, 58
                                                                                                                                                                                                                                                                                  SOFTWAKE: Patentin Ver. 2.0
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TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 54:
                                                                                                                                                                                                    ORGANISM: domo sapiens
1309 ISDVIDYSDEGDSOMOFATYSSSÇÜBÇTEKÇESSSSVNISNEMNEKTESSSPEKPOLIFE 1368
                                           . 78 VNGCPEFRARATAKATVAAFAASEGHSHPR-----
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: #CT/MSv4/04446
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1BM PC compatible
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                                                                                                    14.4%; Score 169; DB 4; Length 2485; 28.4%; Pred. No. 7.96 08;
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US-09-100-804-28
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UE:09 100 804 28
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; Patent No. 6066472
                                                         Query Match 13.4%; Score 156.5; DB 3; Length 73; Best Local Similarity 47.8%; Prod. No. 9.1e-09; Matches 3; Conservative 13; Mismatches 22; Indels
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GOMEZ, LEONEL JORGE APPLICANT: SAKAS, JAN APPLICANT: CLAESSON WELSH, LENA APPLICANT: HELDIN, CARL-HENRIK
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THEE OF INVENTION: EXPRESSION OF BEHAVIORIDE SEQUENCIES FOR MARKET FRONTIER.
TITLE OF INVENTION: TYROSINE PHOSPHATASES
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COMPUTER: IHM PC compatible
OPERATING SYSLEM: PC-DOS/MS-DOS
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Search completed: May 7, 2002, 12:41:41 Job time: 111 sec
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Calitry
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 535-9901
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 13.4%; Score 156.5; DB 1; Length 6.0; Best Local Similarity 27.4%; Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein: 08-410-804-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
PRIOR TOWNTON NUMBER: US 08/259,514
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Type: amino acid
Type: Jipos-
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                                                                                                        161 VSVEGEHHEKAVELLKAAKDSVKLVV 186
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FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
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CITY: San Diego
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C: United States
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4370 La Jolla Village Drive. Ste 700
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